

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2006, 08:47:30 ; Search time 5312 Seconds  
(without alignments)  
11278.802 Million cell updates/sec

Title: US-09-965-703A-3  
Perfect score: 1054  
Sequence: 1 cctgagtgctgtacccga.....gtccggccgctgctctga 1054

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_in.\*
- 3: gb\_env.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_sts.\*
- 11: gb\_sy.\*
- 12: gb\_un.\*
- 13: gb\_vi.\*
- 14: gb\_htg.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1054	100.0	1054	6	AX256355 Sequence
2	1054	100.0	1288	6	AX256353 Sequence
3	1054	100.0	3962	2	CFU29531 Choristoneu
4	1054	100.0	6852	2	AF092030 Choriston
5	1029.4	97.7	1290	6	AX407011 Sequence
6	1010.2	95.8	1073	6	AX407021 Sequence
7	1005	95.4	1110	6	AX256354 Sequence
8	1005	95.4	1542	6	AX256401 Sequence
9	960	91.1	960	6	AX256357 Sequence
10	929	88.1	1247	6	AX256414 Sequence
11	735	69.7	735	6	AX256356 Sequence
12	683.6	64.9	6083	2	AY489269 Plodia in
13	652.4	61.9	1017	2	PCO251809 Precis co
14	636.4	60.4	2126	6	BD224646 Novel ecd
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19	623.4	59.1	2840	6	AX555249 Sequence
20	621.6	59.0	1500	6	AX555315 Sequence
21	621.6	59.0	1767	6	AX555368 Sequence
22	617.4	58.6	1863	6	AX555384 Sequence
23	617.2	58.6	1848	6	AX555382 Sequence
24	617	58.5	1518	6	AX555341 Sequence
25	617	58.5	3972	6	AX555352 Sequence
26	616.4	58.5	1428	6	AX555376 Sequence
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28	614.2	58.3	1515	6	AX555323 Sequence
29	614.2	58.3	1782	6	AX555372 Sequence
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34	605.6	57.5	1500	6	AX555317 Sequence
35	605.6	57.5	1767	6	AX555370 Sequence
36	604	57.3	1524	6	AX555325 Sequence
37	603.2	57.2	1800	6	AX555395 Sequence
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ALIGNMENTS

RESULT 1  
AX256355  
LOCUS AX256355 1054 bp DNA linear PAT 10-OCT-2001  
DEFINITION Sequence 3 from Patent WO0170816.  
ACCESSION AX256355  
VERSION AX256355.1 GI:16075206  
KEYWORDS .  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Palli,S.R., Kapitskaya,M.Z. and Cress,D.E.  
TITLE Bcdysone receptor-based inducible gene expression system  
JOURNAL Patent: WO 0170816-A 3 27-SEP-2001;  
ROHM AND HAAS COMPANY (US)  
FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
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ORIGIN

Query Match	100.0%;	Score 1054;	DB 6;	Length 1054;
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Qy	121	ATGACGTGTGAACCTCCACTCTCTTGAAGCAGCAAGATTCCAGAGTGGTCCCAAGTTT	180	
Db	121	ATGACGTGTGAACCTCCACTCTCTTGAAGCAGCAAGATTCCAGAGTGGTCCCAAGTTT	180	
Qy	181	CTCTCCGACAGCTGTTGGAGACAAACCCGACAGAAAACATCCCGAGTGGAGCCAAC	240	
Db	181	CTCTCCGACAGCTGTTGGAGACAAACCCGACAGAAAACATCCCGAGTGGAGCCAAC	240	

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 361 GACATCTCTTCGCGCAGATCAAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420  
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 1021 ATGCGCGATGCGGCTCCGCGCGCTGCTCTGA 1054  
 Db ATGCGCGATGCGGCTCCGCGCGCTGCTCTGA 1054

RESULT 2

AX256353  
 LOCUS 1288 bp DNA linear PAT 10-OCT-2001  
 DEFINITION Sequence 1 from Patent WO0170816.  
 ACCESSION AX256353  
 VERSION AX256353.1 GI:16075204  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
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 Palli,S.R., Kapitskaya,M.Z. and Cross,D.E.  
 Ecdysone receptor-based inducible gene expression system  
 Patent: WO 0170816-A 1 27-SEP-2001;  
 ROHM AND HAAS COMPANY (US)

FEATURES

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 1. .1288  
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ORIGIN

Query Match 100.0%; Score 1054; DB 6; Length 1288;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-244;  
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CTTGAGTGTGATACCCGAGACTCAGTGCCTCAGTGAAGCGGAAAGAGAACACAG 60  
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 61 AAGGAGAAGGACAAACTGCTGTGACGACGACGCGTGGACGACACATGCCGCCATT 120  
 Db AAGGAGAAGGACAAACTGCTGTGACGACGACGCGTGGACGACACATGCCGCCATT 354  
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 Db GACAGTGTCTGTTGCGGAACCAACGAGGTTACCTCGCGACAACTACCGCAGGCTGGC 834  
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 661 GACAAATCATTAACGCGCTGCTCAGCGTGTGTCATCTTTTCTGACCGGCGAGGTTG 720  
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 Db GAGCAGCGCAACTGTTGGAAGAAATCCAGCGTACTCTGCTGAATACGCTCCGATCTAT 1014  
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 Db ATCTCTCTGAGCTACGACGCTGCGGATCAAAATCCAAATGTCATCTCCCTCAAG 1134  
 901 CTCAAGAACAGAAAGCTGCGGCTTTCTCTGAGAGATCTGGGATGTCGCGGACATGTGCG 960

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Qy 1021 ATGCGCGATGCGGCTGCGGCGCGCTCTGA 1054

Db 1255 ATGCGCGATGCGGCTGCGGCGCGCTCTGA 1288

RESULT 3

LOCUS CFU29531

DEFINITION Choristoneura fumiferana ecdysteroid receptor Ecr-B mRNA, complete cds.

ACCESSION U29531

VERSION U29531.2 GI:5731355

SOURCE

ORGANISM Choristoneura fumiferana (spruce budworm)

Choristoneura fumiferana

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Tortricidae; Tortricinae; Choristoneura.

REFERENCE 1 (bases 1 to 3960)

AUTHORS Kothapalli, R., Palli, S. R., Ladd, T. R., Sohi, S. S., Cress, D., Dhaddalla, T. S., Tzertzinis, G. and Retnakaran, A.

TITLE Cloning and developmental expression of the ecdysone receptor gene from the spruce budworm, Choristoneura fumiferana

JOURNAL Dev. Genet. 17 (4), 319-330 (1995)

REFERENCE 2 (bases 1 to 3960)

AUTHORS Kothapalli, R., Palli, S. R., Ladd, T. and Retnakaran, A.

TITLE Direct Submission

JOURNAL Submitted (20-JUN-1995) Subba Reddy Palli, Molecular Entomology, CFS-Sault Ste. Marie, 1219 Queen Street East, Sault Ste. Marie, ONT P6A 5W7, Canada

REFERENCE 3 (bases 1 to 3960)

AUTHORS Kothapalli, R., Palli, S. R., Ladd, T. and Retnakaran, A.

TITLE Direct Submission

JOURNAL Submitted (12-AUG-1999) Rohm and Haas Research Labs, 727 Norristown Road, PO Box 904, Spring House, PA 19477, USA

REMARK Sequence update by submitter

AUTHORS On Aug 12, 1999 this sequence version replaced gi:3641616.

FEATURES

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ORIGIN

Query Match 100.0%; Score 1054; DB 2; Length 3962;

Best Local Similarity 100.0%; Pred. No. 1.9e-244;

Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 ATGCAAGTGAACCTCCACCTCTGAAGCAGCAAGGATTCACGAAGTGGTCCCAAGTTT 180

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Qy 181 CTCTCCGACAAAGCTGTTGGAGACAAACCCGACAGAAAACATCCCCAGTTTGACAGCCAAC 240

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Qy 241 CAGCAGTTCTTATCGCCAGGCTCATCTGGTACGAGCGGTACGAGCAGCCTTCTGAT 300

Db 1102 CAGCAGTTCTTATCGCCAGGCTCATCTGGTACGAGCGGTACGAGCAGCCTTCTGAT 1161

Qy 301 GAAGATTTGAAGAGATTCAGCAGAGCGTGGCAGCAGCAGCAGTGAAGAGAGTCT 360

Db 1162 GAAGATTTGAAGAGATTCAGCAGAGCGTGGCAGCAGCAGCAGTGAAGAGAGTCT 1221

Qy 361 GACACTCCCTCCGCGCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCGTGAG 420

Db 1222 GACACTCCCTCCGCGCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCGTGAG 1281

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Db 1702 ATCTCTCTGAGCTACGACGCTCGGATGCAAAAATCCAAATGTCATCTCCCTCAAG 1761

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Qy 1021 ATCGCGAGTCCGCGTCCGCGCGCTGCTCTGA 1054



LOCUS AX407011 1290 bp DNA linear PAT 14-JUN-2002  
DEFINITION Sequence 4 from Patent WO0229075.  
ACCESSION AX407011  
VERSION AX407011.1 GI:21439858  
KEYWORDS Choristoneura fumiferana (spruce budworm)  
SOURCE Chorisoneura fumiferana (spruce budworm)  
ORGANISM Chorisoneura fumiferana  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
Tortricidae; Tortricinae; Choristoneura.  
REFERENCE 1  
AUTHORS Palli, S.R., Dhaddialla, T.S., Carlson, G.R., Hormann, R.E., Kudla, A.J.,  
Mohan, P., Cress, D.E. and Herzig, R.P.  
TITLE Multiple inducible gene regulation system  
JOURNAL Patent: WO 0229075-A 4 11-APR-2002;  
ROHM & HAAS (US)  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 97.7%; Score 1029.4; DB 6; Length 1290;  
Best Local Similarity 99.7%; Pred. No. 1.7e-238;  
Matches 1052; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 CCTGAGTGGTGTAGTACCGGACACTCAGTGGCCCATGAAGCGGAAGAGAAAGACACAG 60  
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DB 297 AAGGAGAAGGACAAATGCTGTGTCAGCAGCAGCGGTGGAGCAGCAGCATGCCGCCCAT 356  
QY 121 ATGCAGTGTGAACTTCACTCTGAGAGCAGCAGGATTCAGGAAGTGTCCCAAGGTTT 180  
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QY 241 CAGCAGTTCCTTTATCGCAGGCTCATCTGTGTACAGGACGGGTACGAGCAGCTTCTGAT 300  
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QY 301 GAAGATTGGAAGGATTAACGACAGCTGTGAGCAGCAGCGGACGATGAAGACGAGGTCT 360  
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DB 1256 CATCGCGATGCGCGCTCGCGCGCTGCTCTGA 1290

RESULT 6  
LOCUS AX407021 1073 bp DNA linear PAT 14-JUN-2002  
DEFINITION Sequence 14 from Patent WO0229075.  
ACCESSION AX407021  
VERSION AX407021.1 GI:21439868  
KEYWORDS Choristoneura fumiferana (spruce budworm)  
SOURCE Chorisoneura fumiferana  
ORGANISM Chorisoneura fumiferana  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
Tortricidae; Tortricinae; Choristoneura.  
REFERENCE 1  
AUTHORS Palli, S.R., Dhaddialla, T.S., Carlson, G.R., Hormann, R.E., Kudla, A.J.,  
Mohan, P., Cress, D.E. and Herzig, R.P.  
TITLE Multiple inducible gene regulation system  
JOURNAL Patent: WO 0229075-A 14 11-APR-2002;  
ROHM & HAAS (US)  
FEATURES Location/Qualifiers  
source  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:7141"

ORIGIN

Query Match 95.8%; Score 1010.2; DB 6; Length 1073;  
Best Local Similarity 99.2%; Pred. No. 7.6e-234;  
Matches 1047; Conservative 0; Mismatches 3; Indels 5; Gaps 3;

QY 1 CCTGAGTGGTGTAGTACCGGACACTCAGTGGCCCATGAAGCGGAAGAGAAAGACACAG 60  
DB 1 CCTGAGTGGTGTAGTACCGGACACTCAGTGGCCCATGAAGCGGAAGAGAAAGACACAG 60  
QY 61 AAGGAGAAGGACAAATGCTGTGTCAGCAGCAGCGGTGGAGCAGCAGCATGCCGCCCAT 120  
DB 61 AAGGAGAAGGACAAATGCTGTGTCAGCAGCAGCGGTGGAGCAGCAGCATGCCGCCCAT 120  
QY 121 ATGCAGTGTGAACCTTCACTCTGAGAGCAGGATTCAGGAAGTGTCCCAAGGTTT 180  
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RESULT 7  
AX256354  
LOCUS AX256354 1110 bp DNA linear PAT 10-OCT-2001  
DEFINITION Sequence 2 from Patent WO0170816.  
ACCESSION AX256354  
VERSION AX256354.1 GI:16075205  
KEYWORDS synthetic construct  
SOURCE other sequences; artificial sequences.  
ORGANISM 1  
Palli, S.R., Kapitakaya, M.Z. and Cress, D.E.  
AUTHORS Ecdysone receptor-based inducible gene expression system  
TITLE Patent: WO 0170816-A 2 27-SEP-2001;  
JOURNAL ROHM AND HAAS COMPANY (US)  
FEATURES Location/Qualifiers  
1. .1110  
source

/organism="synthetic construct"  
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Query Match 95.4%; Score 1005; DB 6; Length 1110;  
Best Local Similarity 100.0%; Pred. No. 1.4e-232; Indels 0; Gaps 0;  
Matches 1005; Conservative 0; Mismatches 0;  
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Db 346 CAGCAGTTCCTTATCGCGAGGCTCATCTGTTACCAGGACGGGTACGAGCAGCCTTCTGAT 405  
Qy 301 GAAGATTTCAAGAGGATACGCGAGCGTGGCAGCGGACGATGAAACGGAAGTCT 360  
Db 406 GAAGATTTCAAGAGGATACGCGAGCGTGGCAGCGGACGATGAAACGGAAGTCT 465  
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Qy 541 GACAGTGTCTGTTGCGGACCAAGCGTACACTCGCGACCAACTACCGCAAGGCTGGC 600  
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RESULT 8  
AX256401  
LOCUS AX256401 1542 bp DNA linear PAT 10-OCT-2001  
DEFINITION Sequence 49 from Patent WO0170816.  
ACCESSION AX256401  
VERSION AX256401.1 GI:16075229  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Palli,S.R., Kapitskaya,M.Z. and Cress,D.E.  
TITLE Ecdysone receptor-based inducible gene expression system  
JOURNAL Patent: WO 0170816-A 49 27-SEP-2001;  
ROHM AND HAAS COMPANY (US)  
FEATURES  
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Query Match 95.4%; Score 1005; DB 6; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 1.4e-232;  
Matches 1005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 541 GACAGTGTCTGTTCGGGAAACAAACGAGCTGACACTCGCGACAACTACCGCAAGGCTGGC 600  
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RESULT 9  
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LOCUS AX256357 960 bp DNA linear PAT 10-OCT-2001  
DEFINITION Sequence 5 from Patent WO0170816.  
ACCESSION AX256357  
VERSION AX256357.1 GI:16075208  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Palli,S.R., Kapitskaya,M.Z. and Cress,D.E.  
TITLE Ecdysone receptor-based inducible gene expression system  
JOURNAL Patent: WO 0170816-A 5 27-SEP-2001;  
ROHM AND HAAS COMPANY (US)  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 1.1e-221;  
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Qy 241 CAGCAGTTCCTTATGCGCAGGCTCATCTGTCATCCGAGCGGTGACGAGCGCTTCTGAT 300  
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RESULT 10
AX256414
LOCUS Sequence 62 from Patent WO0170816.
DEFINITION AX256414
ACCESSION AX256414
VERSION AX256414.1 GI:16075239
KEYWORDS
SOURCE
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS Palli,S.R., Kapitskaya,M.Z. and Cress,D.E.
TITLE Ecdysone receptor-based inducible gene expression system
JOURNAL Patent: WO 0170816-A 62 27-SEP-2001;
ROHM AND HAAS COMPANY (US)
FEATURES
Location/Qualifiers
source 1..1247
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Query Match 88.1%; Score 929; DB 6; Length 1247;
Best Local Similarity 100.0%; Pred. No. 3.6e-214;
Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 439 ATGCGAGTGAACCTTCCACTCTCTGAAGCAGCAAGGATTCAGAAAGTGGTCCCAAGGTTT 498
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DB 679 GACACTCCCTTCGCGCAGATCAACAGATGACTATCTCTCAAGTCCAACTTATCTGGGAG 738
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QY |||
QY 901 CTCAAGAACAGAAAGCTGCGCCCTTCTCT 929
DB |||
DB 1219 CTCAAGAACAGAAAGCTGCGCCCTTCTCT 1247

RESULT 11
AX256356
LOCUS Sequence 4 from Patent WO0170816.
DEFINITION AX256356
ACCESSION AX256356
VERSION AX256356.1 GI:16075207
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
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**REFERENCE**  
**AUTHORS** Palli,S.R., Kapitskaya,M.Z. and Cress,D.E.  
**TITLE** Ecdysone receptor-based inducible gene expression system  
**JOURNAL** Patent: WO 0170816-A 4 27-SEP-2001;  
 ROHM AND HAAS COMPANY (US)  
**FEATURES** Location/Qualifiers  
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**ORIGIN**  
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 Best Local Similarity 100.0%; Pred.No. 3.7e-167;  
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 Db 661 GAGGAGATCTGGGATGTGGCGGACATGTGCGACACCCAAACCGCGCTTATCTCTCAGTCC 720  
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VERSION	AY489269.2	GI:45827647
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ORGANISM	Plodia interpunctella	
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REFERENCE	1 (bases 1 to 6083)	
AUTHORS	Slausat,D., Bozzolan,F., Queguiner,I., Porcheron,P. and Debernard,S.	
TITLE	Effects of juvenile hormone on 20-hydroxyecdysone-inducible EcR, HR3, E75 gene expression in imaginal wing cells of Plodia interpunctella lepidoptera	
JOURNAL	Eur. J. Biochem. 271 (14), 3017-3027 (2004)	
PUBMED	15233798	
REFERENCE	2 (bases 1 to 6083)	
AUTHORS	Slausat,D., Debernard,S., Bozzolan,F., Queguiner,I. and Porcheron,P.	
TITLE	Direct Submission	
JOURNAL	Submitted (28-NOV-2003) Laboratoire De Physiologie Cellulaire Des Invertébrés, Université Pierre Et Marie Curie, 12 Rue Cuvier, Paris 75005, France	
REFERENCE	3 (bases 1 to 6083)	
AUTHORS	Slausat,D., Debernard,S., Bozzolan,F., Queguiner,I. and Porcheron,P.	
TITLE	Direct Submission	
JOURNAL	Submitted (30-MAR-2004) Laboratoire De Physiologie Cellulaire Des Invertébrés, Université Pierre Et Marie Curie, 12 Rue Cuvier, Paris 75005, France	
REMARK	Sequence update by submitter	
COMMENT	On Mar 30, 2004 this sequence version replaced gi:40362585.	
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ACCESSION AJ251809  
VERSION AJ251809.1 GI:6580624  
KEYWORDS ecdysteroid receptor; Rcr gene.  
SOURCE Junonia coenia (buckeye)  
ORGANISM Junonia coenia  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
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Papilionoidea; Nymphalidae; Nymphalinae; Junonia.  
1  
REFERENCE  
AUTHORS Reinhardt, R.K., Weber, P. and Koch, P.B.  
TITLE Comparative analysis of ecdysteroid receptor fragments from  
different holometabolous insects  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1017)

AUTHORS Reinhardt, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-1999) Reinhardt R.K., Allgemeine Zoologie und  
Endokrinologie, University of Ulm, Albert-Einstein-Allee 11, 89081  
Ulm, GERMANY  
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DEFINITION Sequence 1 from patent US 6504082.
ACCESSION AR274109
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KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2126)
AUTHORS Albertsen,M.C., Brooke,C.D., Garnaat,C.W. and Roth,B.A.
TITLE    Bcdysone receptors and methods for their use
JOURNAL  Patent: US 6504082-A 1 07-JAN-2003;
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Matches 813; Conservative 0; Mismatches 231; Indels 18; Gaps 2;

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GenCore version 5.1.6  
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2205.350 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1001.8	95.0	1008	8	US-11-118-855-21	Sequence 21, Appl
2	961.2	91.2	2595	6	US-10-888-613B-93	Sequence 93, Appl
3	330.6	31.4	2241	6	US-10-828-831-4	Sequence 4, Appl
4	330.6	31.4	2241	6	US-10-828-831-6	Sequence 6, Appl
5	330.6	31.4	2241	6	US-10-828-831-8	Sequence 8, Appl
6	125.4	11.9	1383	8	US-11-076-163-6	Sequence 6, Appl
7	125.4	11.9	1959	8	US-11-136-527-2980	Sequence 2980, Ap
8	125.4	11.9	2033	8	US-11-166-412-18	Sequence 18, Appl
9	94.4	9.0	1344	8	US-11-076-163-2	Sequence 2, Appl
10	94.4	9.0	1528	8	US-11-166-412-2	Sequence 2, Appl
11	75.8	7.2	2156	8	US-11-136-527-2936	Sequence 2936, Ap
12	74	7.0	2329	8	US-11-136-527-1966	Sequence 1966, Ap
13	67.6	6.4	2355	8	US-11-112-908-15	Sequence 15, Appl
14	66.2	6.3	1400	8	US-11-136-527-4435	Sequence 4435, Ap
15	66.2	6.3	1723	8	US-11-136-527-339	Sequence 339, App
16	61.2	5.8	1775	8	US-11-136-527-4037	Sequence 4037, Ap
17	56.4	5.4	4550	8	US-11-136-527-1874	Sequence 1874, Ap
18	54.2	5.1	2043	8	US-11-136-527-2325	Sequence 2325, Ap
19	53.6	5.1	3119	8	US-11-000-688-398	Sequence 398, App
20	50.4	4.8	3923	8	US-11-136-527-3450	Sequence 3450, Ap
21	45.4	4.3	600	8	US-11-136-527-7076	Sequence 7076, Ap
22	45.2	4.3	2007	8	US-11-136-527-1897	Sequence 1897, Ap

23	44.4	4.2	1400	8	US-11-136-527-7923	Sequence 7923, Ap
24	44.4	4.2	2070	8	US-11-136-527-3827	Sequence 3827, Ap
25	44.4	4.2	3518	8	US-11-136-527-2799	Sequence 2799, Ap
26	42.2	4.0	2130	8	US-11-136-527-2138	Sequence 2138, Ap
27	41	3.9	600	8	US-11-136-527-4470	Sequence 4470, Ap
c 28	41	3.9	852	8	US-11-136-527-374	Sequence 374, App
29	40.4	3.8	806	8	US-11-112-908-398	Sequence 398, App
c 30	40.4	3.8	1135	8	US-11-112-908-404	Sequence 404, App
31	40.4	3.8	161994	8	US-11-112-908-57	Sequence 57, Appl
c 32	40.4	3.8	161994	8	US-11-112-908-57	Sequence 57, Appl
33	40.4	3.8	168656	8	US-11-112-908-59	Sequence 59, Appl
c 34	40.4	3.8	168656	8	US-11-112-908-59	Sequence 59, Appl
35	40.4	3.8	170285	8	US-11-112-908-58	Sequence 58, Appl
c 36	40.4	3.8	170285	8	US-11-112-908-58	Sequence 58, Appl
37	40.2	3.8	45	8	US-11-118-855-147	Sequence 147, App
c 38	40.2	3.8	45	8	US-11-118-855-148	Sequence 148, App
39	40.2	3.8	600	8	US-11-136-527-5092	Sequence 5092, Ap
40	40.2	3.8	1251	8	US-11-136-527-996	Sequence 996, App
41	37.2	3.5	42	8	US-11-118-855-103	Sequence 103, App
c 42	37.2	3.5	42	8	US-11-118-855-104	Sequence 104, App
43	37	3.5	40	8	US-11-118-855-133	Sequence 133, App
c 44	37	3.5	40	8	US-11-118-855-134	Sequence 134, App
45	37	3.5	5251	8	US-11-166-412-13	Sequence 13, Appl

#### ALIGNMENTS

##### RESULT 1

US-11-118-855-21  
; Sequence 21, Application US/11118855  
; Publication No. US20050266457A1  
; GENERAL INFORMATION:  
; APPLICANT: Palli, Subba Reddy  
; APPLICANT: Kumar, Mohan  
; TITLE OF INVENTION: Mutant Receptors and Their Use in a Nuclear Receptor-Based  
; FILE OF INVENTION: Inducible Gene Expression System  
; FILE REFERENCES: A01508-US  
; CURRENT APPLICATION NUMBER: US/11/118,855  
; CURRENT FILING DATE: 2005-04-28  
; PRIOR FILING DATE: 2004-04-30  
; PRIOR FILING DATE: 2004-04-30  
; PRIOR APPLICATION NUMBER: US 60/609,424  
; PRIOR FILING DATE: 2004-09-13  
; NUMBER OF SEQ ID NOS: 176  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 21  
; LENGTH: 1008  
; TYPE: DNA  
; ORGANISM: Choriostoneura fumiferana  
US-11-118-855-21

Query Match	95.0%	Score	1001.8	DB	8	Length	1008
Best Local Similarity	99.8%	Pred. No.	2.9e-272				
Matches	1003	Conservative	0	Mismatches	2	Indels	0
Gaps	0						
Qy	1	CCTGAGTCGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAGAGAAAGCAG	60				
Db	4	CCTGAGTCGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAGAGAAAGCAG	63				
Qy	61	AAGGAGAGGACAACTGCTGTGACGACGAGCGGTGACGACCAATGCCGCCCAT	120				
Db	64	AAGGAGAGGACAACTGCTGTGACGACGAGCGGTGACGACCAATGCCGCCCAT	123				
Qy	121	ATGCACTGTGAACCTCCACTCTCTGAGGAGAGGATTCACGAGTGGTCCCAAGTTT	180				
Db	124	ATGCACTGTGAACCTCCACTCTCTGAGGAGAGGATTCACGAGTGGTCCCAAGTTT	183				
Qy	181	CTCTCCGACAAAGCTGTTGGAGACAAACCCGACAGAAACATCCCCAGTTTGACAGCAAC	240				
Db	184	CTCTCCGACAAAGCTGTTGGAGACAAACCCGACAGAAACATCCCCAGTTTGACAGCAAC	243				
Qy	241	CAGCAGTTTCTTATCGCCAGGCTCATCTGTGTACGAGCGGTACGAGCAGCCTTCTGAT	300				

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Db 244 CAGCAGTTCCTATGCGCAGGCTCACTGGTACCGAGCGGTACGAGCAGCCTTCTGAT 303
Qy 301 GAAGATTGGAAGGATTACGAGAGCGTGGCAGCAAGCGGAGCGATGAAACGAAGAGTCT 360
Db 304 GAAGATTGGAAGGATTACGAGAGCGTGGCAGCAAGCGGAGCGATGAAACGAAGAGTCT 363
Qy 361 GACACTCCCTTCGCGCAGATCAAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420
Db 364 GACACTCCCTTCGCGCAGATCAAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 423
Qy 421 TTCGCAAGGGATTGCGCAGGTTGCGCAAGATCTCGCAGCGCTGATCAAAATTACGCTGCTT 480
Db 424 TTCGCAAGGGATTGCGCAGGTTGCGCAAGATCTCGCAGCGCTGATCAAAATTACGCTGCTT 483
Qy 481 AAGGCTTGCTCAAGTAGGTAATGATGCTCCGAGTCCGCGAGATCGATCGAGTCCGCGCTCA 540
Db 484 AAGGCTTGCTCAAGTAGGTAATGATGCTCCGAGTCCGCGAGATCGATCGAGTCCGCGCTCA 543
Qy 541 GACAGTGTTCGTTCCGGAACCAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 600
Db 544 GACAGTGTTCGTTCCGGAACCAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 603
Qy 601 ATGGCCTTACGTCATCGAGGATCTACTGCACTTCTGCGGTCGATGACTCTATGGGCTTG 660
Db 604 ATGGCCTTACGTCATCGAGGATCTACTGCACTTCTGCGGTCGATGACTCTATGGGCTTG 663
Qy 661 GACAACTCATTACGCGCTGCTCAGCGTGTGCTCATCTTTCTGACCGGCGCAGGCTTG 720
Db 664 GACAACTCATTACGCGCTGCTCAGCGTGTGCTCATCTTTCTGACCGGCGCAGGCTTG 723
Qy 721 GAGCAGCGCAACTGTTGGGAAGAAATCCAGCGGTACTACCTGAATAGCGTCCGCACTAT 780
Db 724 GAGCAGCGCAACTGTTGGGAAGAAATCCAGCGGTACTACCTGAATAGCGTCCGCACTAT 783
Qy 781 ATCTCTGAACCAAGTACGCGGTCGCGGCTTCTGCGTCAATACGGAAGATCTCTCTCA 840
Db 784 ATCTCTGAACCAAGTACGCGGTCGCGGCTTCTGCGTCAATACGGAAGATCTCTCTCA 843
Qy 841 ATCTCTCTGAGCTACGCAAGCTCGGATCGCAAACTCCAACTATGTCATCTCCCTCAAG 900
Db 844 ATCTCTCTGAGCTACGCAAGCTCGGATCGCAAACTCCAACTATGTCATCTCCCTCAAG 903
Qy 901 CTCAAGAACGAAGCTGCGGCTTCTCGAGGATCTGGGATGTTGGGAGCATGTGCG 960
Db 904 CTCAAGAACGAAGCTGCGGCTTCTCGAGGATCTGGGATGTTGGGAGCATGTGCG 963
Qy 961 CACACCAACGCGCGCTATCTCGAGTCCGCCCAAGATCTCTAG 1005
Db 964 CACACCAACGCGCGCTATCTCGAGTCCGCCCAAGATCTCTAG 1008

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RESULT 2

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US-10-888-613B-93
; Sequence 93, Application US/10888613B
; Publication No. US20060008911A1
; GENERAL INFORMATION:
; APPLICANT: Donald Danforth Plant Science Center
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING GENE EXPRESSION IN PLANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 0104850
; CURRENT APPLICATION NUMBER: US/10/888,613B
; CURRENT FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 93
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: This sequence was artificially derived and/or created by the
; OTHER INFORMATION: inventors.
US-10-888-613B-93

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Query Match 91.2%; Score 961.2; DB 6; Length 2595;
Best Local Similarity 99.2%; Pred. No. 1.2e-260;
Matches 998; Conservative 0; Mismatches 3; Indels 5; Gaps 3;
Qy 1 CTTGAGTGGTGTAGTACCCGAGACTCAGTGGCGCATGAGCGGAAAGAGAAAGACACAG 60
Db 751 CTTGAGTGGTGTAGTACCCGAGACTCAGTGGCGCATGAGCGGAAAGAGAAAGACACAG 810
Qy 61 AAGGAGAAGGACAAACTGCTGTGACGACGACGAGGTGGAGCAGACCATGCGGCCATT 120
Db 811 AAGGAGAAGGACAAACTGCTGTGACGACGACGAGGTGGAGCAGACCATGCGGCCATT 870
Qy 121 ATGCAGTGTGAACCTCCACTCTCTGAGCAGCAGAGGATTCACGAGTGTGTCGAGGTTT 180
Db 871 ATGCAGTGTGAACCTCCACTCTCTGAGCAGCAGAGGATTCACGAGTGTGTCGAGGTTT 930
Qy 181 CTCTCCGACAAAGCTGTTGGAGACAAACCGGAGAAAACATCCCCAGTTTGACAGCAAC 240
Db 931 CTCTCCGACAAAGCTGTTGGAGACAAACCGGAGAAAACATCCCCAGTTTGACAGCAAC 990
Qy 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTTACCGAGCAGCGGTACGAGCAGCCTTCTGAT 300
Db 991 CAGCAGTTCCTTATCGCCAGGCTCATCTGTTACCGAGCAGCGGTACGAGCAGCCTTCTGAT 1050
Qy 301 GAAGATTGGAAGGATTACGAGAGCGTGGCAGCAAGCGGACGATGAAAACGAAGAGTCT 360
Db 1051 GAAGATTGGAAGGATTACGAGAGCGTGGCAGCAAGCGGACGATGAAAACGAAGAGTCT 1110
Qy 361 GACACTCCCTTCGCGCAGATCAAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420
Db 1111 GACACTCCCTTCGCGCAGATCAAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 1170
Qy 421 TTGCGAAGGGATTGCGCAGGTTGCGCAAGATCTCGCAGCCTGATCAAAATTACGCTGCTT 480
Db 1171 TTGCGAAGGGATTGCGCAGGTTGCGCAAGATCTCGCAGCCTGATCAAAATTACGCTGCTT 1230
Qy 481 AAGGCTTGCTCAAGTAGGTAATGATGCTCCGAGTCCGCGAGCAGTACGATGCGGCTCA 540
Db 1231 AAGGCTTGCTCAAGTAGGTAATGATGCTCCGAGTCCGCGAGTCCGCGCTCA 1287
Qy 541 GACAGTGTTCGTTCCGGAACCAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 600
Db 1288 GACAGTGTTCGTTCCGGAACCAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 1347
Qy 601 ATGGCCTTACGTCATCGAGGATCTACTGCACTTCTGCGGTCGATGACTCTATGGCGTTG 660
Db 1348 ATGGCCTTACGTCATCGAGGATCTACTGCACTTCTGCGGTCGATGACTCTATGGCGTTG 1407
Qy 661 GACAACTCATTACGCGCTGCTCAGCGGTGTCATCTTTCTGACCGGCGCAGGTTG 720
Db 1408 GACAACTCATTACGCGCTGCTCAGCGGTGTCATCTTTCTGACCGGCGCAGGTTG 1467
Qy 721 GAGCAGCGCAACTGTTGGGAAGAAATCCAGCGGTACTACTGAATACGCTCCGCACTAT 780
Db 1468 GAGCAGCGCAACTGTTGGGAAGAAATCCAGCGGTACTACTGAATACGCTCCGCACTAT 1527
Qy 781 ATCTCTGAACCAAGCTGAGCGGTCGCGGCTTCTGCGTCAATATACGCGCAAGATCTCTCA 840
Db 1528 ATCTCTGAACCAAGCTGAGCGGTCGCGGCTTCTGCGTCAATATACGCGCAAGATCTCTCA 1587
Qy 841 ATCTCTCTGAGCTACGCAAGCTCGCGCATGCAAACTCCAACTATGTCATCTCCCTCAAG 900
Db 1588 ATCTCTCTGAGCTACGCAAGCTCGCGCATGCAAACTCCAACTATGTCATCTCCCTCAAG 1647
Qy 901 CTCAAGAACGAAGCTGCGGCTTCTCGAGGATCTGGGATGTTGGGAGCATGTGCG- 959
Db 1648 CTCAAGAACGAAGCTGCGGCTTCTCGAGGATCTGGGATGTTGGGAGCATGTGCG- 1707
Qy 960 GCACACCAACCGCGCTATCTCGAGTCCGCCCAAGATCTCTAG 1005
Db 1708 GCACACCAACCGCGCTAT-CTCGAGTCCGCCCAAGATCTCTAG 1752

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## RESULT 3

US-10-828-831-4  
; Sequence 4, Application US/10828831  
; Publication No. US20060014711A1  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, RONALD M.  
; APPLICANT: NO, DAVID  
; APPLICANT: SAEZ, ENRIQUE  
; TITLE OF INVENTION: METHODS FOR MODULATING EXPRESSION OF EXOGENOUS GENES IN  
; FILE REFERENCE: SALK1520-2  
; CURRENT APPLICATION NUMBER: US/10/828,831  
; CURRENT FILING DATE: 2004-04-20  
; PRIOR APPLICATION NUMBER: US/09/042,488  
; PRIOR FILING DATE: 1998-03-16  
; PRIOR APPLICATION NUMBER: 08/974,530  
; PRIOR FILING DATE: 1997-11-19  
; PRIOR APPLICATION NUMBER: 08/628,830  
; PRIOR FILING DATE: 1996-04-05  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 2241  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant  
; OTHER INFORMATION: VgEcr  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2238)  
US-10-828-831-4

Query Match 31.4%; Score 330.6; DB 6; Length 2241;  
Best Local Similarity 59.5%; Pred. No. 4.1e-83;  
Matches 617; Conservative 0; Mismatches 384; Indels 36; Gaps 2;

Qy 1 CCTGAGTGCCTAGTACCCGAGACTCAGTGCCTCCATGAAGCGGAAAGAGAAAGACAG 60  
Db 595 CCGGAATGCGTCTGCGGAGAACCAATGTGCGATGAAGCGCGGCGGAAAGAGCCAG 654  
Qy 61 AAGGAGAAGGACAAATGCTGTCGAGCAGCAGCGGTGAGAGCAACATGCCGCCATT 120  
Db 655 AAGGAGAAGGACAAATGATGACCTTCCGCGAGCTCTCAGCATGCGGCAATGGCAGCTTG 714  
Qy 121 ATGCAAGTGTGAACCTCCACTCTCGAGCAGCAGGATTCAGAGTGGTCCAG---- 176  
Db 715 GCCTCTGCTGCGCGCCAGACTTTGTTAAGAAAGAGATTTCTTGACCTTATGACATCGAG 774  
Qy 177 -----GTTTCTCTCCGACAACTGTTGGAGACAAACCGCGAG 213  
Db 775 CCGCCCCAGCATGCCACTATTCGCTACTACTGATGAATATTTGGCCAGTGTCAAGCG 834  
Qy 214 AAAAATATCCCCAGTTGAGCAACAGCAGATTCCTTATCGCAGGCTCATCTGGTAC 273  
Db 835 CGCAATATATCTCTTAAACGTACAAATCAGTTGCGCGGTTATATACAAAGTTAAATTTGGTAC 894  
Qy 274 CAGACCGGTACGAGCAGCTCTGATGAAGATTTGAAGAGATTACGACAGCTGGCAG 333  
Db 895 CAGATGGCTATGACGAGCCATCTGAAGAGATCTCAGGCGTAAATGAGT----- 945  
Qy 334 CAAGCGGACGATGAAGAGAGTCTGACACTCCCTTCGCCAGATCAGAGATGACT 393  
Db 946 CAACCCGATGAAGAGAGAGCAACGAGCTGAGCTTTCGGCATATTAACGAGATACC 1005  
Qy 394 ATCTCTACGGTCCAACTTATCGTGGAGTTCCGAGGAGATTGCCAGGTTCCGCAAGATC 453  
Db 1006 ATACTCAGGTCAGTTGATTTGTTGAGTTTCTAAAGGTCTACCAAGGTTTACAAAGATA 1065  
Qy 454 TCGCAGCTGATCAATTAAGCTGCTTAAAGCTTCTCAAGTGAAGTAAATGATGCTCGA 513  
Db 1066 CCCAGGAGGACGATCAGCTTAAAGGCTGCTCGTGGAGGTGATGATGCTGCT 1125

Qy 514 GTCCGCGACGATACGATGCGGCTCAGACAGTGTCTTGTTTCGGAACAACCAAGCGTAC 573  
Db 1126 ATGGCAGCAGCTATGACCAAGCTCGGACTCAATATTTCTTCGGAATAATAGATCATAT 1185  
Qy 574 ACTCGGACAACTACCGCAAGGCTGGCATGCGCTACGTCATCGAGGATCTACTGCACTTC 633  
Db 1186 ACGCGGATTTCTTACAAATATGCGCGAATGGCTGATTAACATTTGAAGACCTCTGCAATTC 1245  
Qy 634 TGCCGCTGATGTACTCTATGGCGTTCGACAAATCCATTAACGCTGCTCAGCGCTGTC 693  
Db 1246 TGCGGCCAATGTTCTCGATGAAGTGGACAACTCGAATACGCGCTTCTCACTGCCATT 1305  
Qy 694 GTCACTTTTCTGACCGGCCAGGGTTGGAGCAGCGCCAACTGGTGGAGAATAATCCAGCG 753  
Db 1306 GTGATCTTCTCGACCGCGCGGCTCGAGAAGGCCCAACTAGTTCGAAGCGATCCAGAGC 1365  
Qy 754 TACTACTGATACGCTCCGATCTATATCTGAACAGCTGAGCGGGTGGCGGCTTCG 813  
Db 1366 TACTACTGACACGCTACGCAATTTATATCTAACCGCCACTCGCGCGACTCAATGAGC 1425  
Qy 814 TCCGTATATACGCAAGATCTCTCAATCTCTCTGAGCTACGACGCTCGGCATGCAA 873  
Db 1426 CTGCTCTTACGCAAGCTGCTCTCGATCTCTACCGAGCTCGCTAGCTGGGCAACG 1485  
Qy 874 AACTCCAACATGTGCATCTCCCTCAAGCTCAAGAACAGAAAGTSCCGCTTTCTCTCGAG 933  
Db 1486 AAGCGCAGATGTGTTTCTCACTAAAGCTCAAAACCGCAACTGCCCAAGTTCCTCGAG 1545  
Qy 934 GAGATCTGGATGCGGAGCATGTCCGACACCCACCAACCGCGGCTATCTCGAGTCCCCC 993  
Db 1546 GAGATCTGGAGCTTCATGCCATCCCGCATCGGTCCAGTCCGACCTTCAGATTACCCAG 1605  
Qy 994 ACGAATCTTAGCCCT 1010  
Db 1606 GAGGAGAACGAGCGTCT 1622

## RESULT 4

US-10-828-831-6  
; Sequence 6, Application US/10828831  
; Publication No. US20060014711A1  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, RONALD M.  
; APPLICANT: NO, DAVID  
; APPLICANT: SAEZ, ENRIQUE  
; TITLE OF INVENTION: METHODS FOR MODULATING EXPRESSION OF EXOGENOUS GENES IN  
; FILE REFERENCE: SALK1520-2  
; CURRENT APPLICATION NUMBER: US/10/828,831  
; CURRENT FILING DATE: 2004-04-20  
; PRIOR APPLICATION NUMBER: US/09/042,488  
; PRIOR FILING DATE: 1998-03-16  
; PRIOR APPLICATION NUMBER: 08/974,530  
; PRIOR FILING DATE: 1997-11-19  
; PRIOR APPLICATION NUMBER: 08/628,830  
; PRIOR FILING DATE: 1996-04-05  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 2241  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant  
; OTHER INFORMATION: VpEcr  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2238)  
US-10-828-831-6

Query Match 31.4%; Score 330.6; DB 6; Length 2241;  
Best Local Similarity 59.5%; Pred. No. 4.1e-83;



Matches 617; Conservative 0; Mismatches 384; Indels 36; Gaps 2;	
Qy	1 CCTGAGTGGCTAGTACCGGAGACTCAGTGGCCGATGAAGCGGAAAGAGAAAGACACAG 60
Db	595 CCGGAATGCGTCTCCGGGAGAACCAATGTGCGATGAAGCGGCGGAAAGAGAGGCCAG 654
Qy	61 AAGGAGAAGGACAAATCGCTGTGAGCAGCAGCAGCGGTGGACGACCAATCGCCGCCATT 120
Db	655 AAGGAGAAGGACAAATGACACTCTGCGCGAGCTCTCAGCATGGCGGCAATGGCAGCTTG 714
Qy	121 ATGACAGTGAACCTCCACCTCCTGAAGCAGCAAGGATTCACGAAGTGGTCCCAAG--- 176
Db	715 GCCTCTGGTGGCGCAAGACTTTGTTAAGAGGAGATTCTTGACCTTATGACATGGAG 774
Qy	177 -----GTTTCTCTCCGACAGCTGTGGAGGATTTGGCGCAAAACCGGCAG 213
Db	775 CCGCCCCAGCATGCCACTATTCGCGTACTACCTGATGAATAATTGGCCAAGTGTCAAGCG 834
Qy	214 AAAAAATCCCCAGTTTGACAGCCACCGACAGTTCCTTATCGCCAGGCTCATCTGTATC 273
Db	835 CGCATATACCTCTTAAAGTACATCAGTTGGCCGTTATATACAAAGTTAAATTTGGTAC 894
Qy	274 CAGGACGGGTACGAGCAGCTTCTGATGAAGATTTGAAGAGGATTTACGCAAGCTGGCAG 333
Db	895 CAGGATGGCTATGAGCAGCCACTGTAAGAGGATCTCAGGCGTATATAGT----- 945
Qy	334 CAAGCGGACGATGAAGAGAGTCTGACACTCCCTTCGCGCAGATCACAGAGATGACT 393
Db	946 CAACCCGATGAGACGAGAGCCAAACCGACGTGCTTCGCGCATATAACCGAGATAACC 1005
Qy	394 ATCTCTACCGTCCAACTTATCGTGGAGTTCGGAAGGATTTGCCAGGTTTCGCAAGATC 453
Db	1006 ATACTCAGGTCGAGTTGATTTGAGTTTGCTAAAGTCTTACAGGCTTACAAAGATA 1065
Qy	454 TCGCAGCTGATCAAAATTAACGCTCTTAAGGCTTGCTCAAGTGAAGTAAATGATGCTCCGA 513
Db	1066 CCCAGGAGGACCATGATCACTTAAAGGCTGCTCGTGGAGGTGATGATGCTCGT 1125
Qy	514 GTGCGGAGATACGATGCGGCTCAGACAGTGTCTGTTCGGGAACCAACCAAGGTAC 573
Db	1126 ATGGCAGAGCGCTATGACCAAGCTCGGACTCAATATTTCTCGGAATAATAGATCATAT 1185
Qy	574 ACTCGGACAACTACCGAAGGCTGGCATCGCTACGTATCAGGAGTCTACTGCATTC 633
Db	1186 ACGGGAATTTTACAAAATGCGCGAATGGCTGATTAACATTGAAGACCTGTGCTATTC 1245
Qy	634 TGGCGGTGATGATCTATATGGCGTTGGACAAACATCCATTACGCGCTGTCTCAGCGCTGC 693
Db	1246 TGGCGCAAAATGTTCTCGATGAAGGTGACAAAGTCAAGTCACTGCTTCTCACTGCCATT 1305
Qy	694 GTCATCTTTTCTGACCGGCGAGGTTGGAGAGCGCGCACTGGTGGAGAAATCCAGCGG 753
Db	1306 GTGATCTTCTCGGACCGCGCGGCTCTGGAGAGGCCCACTAGTTCGAAGCGATCCAGAGC 1365
Qy	754 TACTTACGTGAATACGCTCCGATCTATATCTGAACAGCTGAGCGGCTGGCGGCTTCG 813
Db	1366 TACTATGATGACAGCTACGATTTATATCTCAACCGCATCTGCGCGGACTCAATGAGC 1425
Qy	814 TCGGTCTATATACGCAAGATCTCTCAATCTCTCTGAGCTACGACGCTCGGCATGCAA 873
Db	1426 CTGCTCTTACGCAAAAGCTCTCTCGATCTCTCAACCGAGCTGGCTACGCTGGGCAACAG 1485
Qy	874 AACTCGAATGTCATCTCGCTCAAGCTCAGAAAGAGCTGGCGCTTCCTCTGAG 933
Db	1486 AAGCCGAGATGTGTTTCTCACTAAAGCTCAAAAACCGCAAACTGCGCCAAAGTTCTCGAG 1545
Qy	934 GAGATCTGGGATGTGGCGGACATGTGCGCACACCAACCGCGCTATCTCTCGAGTCCCC 993
Db	1546 GAGATCTGGGAGCTTCAATGCCATCCCCCATCGGTCCAGTCCGACCTTCAGATTACCCAG 1605
Qy	994 ACGAATCTTAGCCCCCT 1010
Db	1606 GAGGAGAACGAGCTCT 1622

RESULT 5

US-10-828-831-8  
 ; Sequence 8, Application US/10828831  
 ; Publication No. US20060014711A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EVANS, RONALD M.  
 ; APPLICANT: NO, DAVID  
 ; APPLICANT: SAEZ, ENRIQUE  
 ; TITLE OF INVENTION: METHODS FOR MODULATING EXPRESSION OF EXOGENOUS GENES IN  
 ; TITLE OF INVENTION: MAMMALIAN SYSTEMS, AND PRODUCTS REALIZED THEREO  
 ; FILE REFERENCE: SALX1520-2  
 ; CURRENT APPLICATION NUMBER: US/10/828,831  
 ; CURRENT FILING DATE: 2004-04-20  
 ; PRIOR APPLICATION NUMBER: US/09/042,488  
 ; PRIOR FILING DATE: 1998-03-16  
 ; PRIOR APPLICATION NUMBER: 08/974,530  
 ; PRIOR FILING DATE: 1997-11-19  
 ; PRIOR APPLICATION NUMBER: 08/628,830  
 ; PRIOR FILING DATE: 1996-04-05  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 8  
 ; LENGTH: 3126  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Recombinant  
 ; OTHER INFORMATION: GECR  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(3123)  
 ; US-10-828-831-8

Query Match 31.4%; Score 330.6; DB 6; Length 3126;	
Best Local Similarity 59.5%; Pred. No. 4.7e-83; Indels 36; Gaps 2;	
Matches 617; Conservative 0; Mismatches 384; Indels 36; Gaps 2;	
Qy	1 CCTGAGTGGCTAGTACCGGAGACTCAGTGGCCGATGAAGCGGAAAGAGAAAGACACAG 60
Db	1480 CCGGAATGCGTCTCCGGGAGAACCAATGTGCGATGAAGCGGCGGAAAGAGGCCAG 1539
Qy	61 AAGGAGAAGGACAACTGCTGTGACGACGACGAGCGGTGACGACCAATGCGCCCATTT 120
Db	1540 AAGGAGAAGGACAAATGACCACTTCGCGAGCTCTCAGCATGGCGGCAATGGCAGCTTG 1599
Qy	121 ATGACAGTGTGAACCTCCACTCTCTGAAGCAGCAAGGATTCACGAAGTGGTCCCAAG--- 176
Db	1600 GCCTCTGGTGGCGGCCAAGACTTTGTTAAGAGGAGATTTCTGACCTTATGACATGGAG 1659
Qy	177 -----GTTTCTCTCCGACAGCTGTGGAGACAAACCGGCAG 213
Db	1660 CGGCCCCAGCATGCCACTATTCGCTACTACTGATGAATAATTGGCCAAGTGTCAAGCG 1719
Qy	214 AAAAAATCCCCAGTTTGACAGCCACCGACAGTTCCTTATCGCCAGGCTCATCTGTGATC 273
Db	1720 CGCAATATACCTTCTCTTAAAGCTCAATCAGTTGGCGGTTATATACAAAGTTAAATTTGGTAC 1779
Qy	274 CAGGACGGGTACGAGCAGCTTCTGATGAAGATTTTGAAGAGGATTTACGCAAGCTGGCAG 333
Db	1780 CAGATGGCTATGAGCAGCCATCTGAAGAGGATCTCAGCGGTATATATAGT----- 1830
Qy	334 CAAGCGGACGATGAAGAAACGAAGAGTCTGACACTCCCTTCGCGCAGATCACAGAGATGACT 393
Db	1831 CAACCCGATGAGAACGAGAGCCAAACCGAGCTCAGCTTTCGCGCATATATACCGAGATAACC 1890
Qy	394 ATCTCTACCGTCCAACTTATCGTGGAGTTTCGCAAGGATTTGCCAGGTTTCGCAAGATC 453
Db	1891 ATACTCAGGTCGAGTTGATTTGATTTGCTTAAAGGTTTGTCTAAAGGCTTACACGCGTTTACAAAGATA 1950
Qy	454 TCGCAGCTGATCAAAATTAAGCTTGAAGGCTTGTCTCAAGTGAAGTAAATGATGCTCCGA 513

Db 1951 CCCAGGAGGACAGATCAGTTACTAAAGGCTCTGTCGAGGAGTGAATGATGCTGCGT 2010  
 Qy 514 GTGCGCGCAGATAGATGCGGCTCTCAGACAGTGTCTGTTGCGCAACAAACCAACGCTAC 573  
 Db 2011 ATGGCAGCAGGCTATGACACACAGCTCGGACTCAATATTCTTCGCGAATAATAGATCATAT 2070  
 Qy 574 ACTCGCGCACTACCGCAGGCTGGCATGGCTAGCTAGCTATCGAGGATCTACTGCACTTC 633  
 Db 2071 ACGCGGGAATCTTACAAAATGSCCGGAATGGCTGATTAACATTTGAAGACCTGCTGCAATTC 2130  
 Qy 634 TGCGCGTGCATGATCTCTATGSCGTTGGACACATCCATTACGCGCTCTCAGCGCTGTC 693  
 Db 2131 TGCGCGCAATGTTCTCGATGAAGTGGACACGTCGAATACGCGCTCTCTACTGCCATT 2190  
 Qy 694 GTCACTTTTCTGACCGCGCAGGTTGGAGCAGCGCAACTGGTGGAAAGAAATCCAGCGG 753  
 Db 2191 GTGATCTTCTCGGACCGCGCGGCTCGAGAGGCCCACTAGTCGAAGCGATCCAGAGC 2250  
 Qy 754 TACTACCTGAATACGCTCGGATCTATATCTGGAACAGCTAGCGGGTGGCGCGGTTGCG 813  
 Db 2251 TACTACATCGACACGCTAGCATGATTTATATCTCAACCGCCACTGCGCGGACTCAATGAGC 2310  
 Qy 814 TCCGTCATATAGCGCAAGATCTCTCAATCTCTGAGCTACGACGCTCGGCAATGCAA 873  
 Db 2311 CTGCTCTTCTAGCAAGCTGCTCTCGATCTCTCAGATCTCAACCGGCTGCTGAGCAG 2370  
 Qy 874 AACTCCAACTGTGATCTCCCTCAAGCTCAAGAAACAGAAAGCTCCGCGCTTTCTCGAG 933  
 Db 2371 AACCGCGAGATGTTCTCTCAATAGCTCAAAACCGCAACTGCCCCAAGTTCTCTGAG 2430  
 Qy 934 GAGATCTGGATGTGGCGACATGTCGACACCCCAACCGCGCTCTATCTCGAGTCCCCC 993  
 Db 2431 GAGATCTGGGACGTTTCATGCCATCCGCTCCGATCGGTCAGTCCGACCTTCAGATTACCCAG 2490  
 Qy 994 ACGAATCTAGCCCT 1010  
 Db 2491 GAGGAAACGAGCGTCT 2507  
 RESULT 6  
 US-11-076-163-6  
 ; Sequence 6, Application US/11076163  
 ; Publication No. US20050261319A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Deuschle, Ulrich  
 ; APPLICANT: Loebbert, Ralph  
 ; APPLICANT: Blume, Beatriz  
 ; APPLICANT: Koegi, Manfred  
 ; APPLICANT: Kremoser, Claus  
 ; APPLICANT: Kober, Ingo  
 ; APPLICANT: Bauer, Ulrike  
 ; APPLICANT: Hermann, Kristina  
 ; APPLICANT: Albers, Michael  
 ; TITLE OF INVENTION: Novel 2-amino-4-quinazolinones and 2-amino-4-oxoquinazolinones as  
 ; TITLE OF INVENTION: LXR Nuclear Receptor Binding Compounds with Partial Agonistic  
 ; TITLE OF INVENTION: Properties  
 ; FILE REFERENCE: BB-139  
 ; CURRENT APPLICATION NUMBER: US/11/076,163  
 ; CURRENT FILING DATE: 2005-03-09  
 ; PRIOR APPLICATION NUMBER: PCT/EP03/10036  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: PCT/EP03/07067  
 ; PRIOR FILING DATE: 2003-07-02  
 ; PRIOR APPLICATION NUMBER: EP 02020255.2  
 ; PRIOR FILING DATE: 2002-09-10  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: Patent in version 3.3  
 ; SEQ ID NO 6  
 ; TYPE: DNA  
 ; LENGTH: 1383  
 ; ORGANISM: Homo sapiens  
 US-11-076-163-6

Query Match 11.9%; Score 125.4; DB 8; Length 1383;  
 Best Local Similarity 54.7%; Pred. No. 2e-25;  
 Matches 321; Conservative 0; Mismatches 251; Indels 15; Gaps 3;  
 Qy 367 CCCTTCGCGCAGATCAGAGATGACTATCTCAGGTCCTCAACTTATGCTGGAGTTGCGG 426  
 Db 796 CGCTTTCGCCACTTTCAGGAGCTGGCCATCTCAGTCCAGGAGATCGTGGACTTCGCT 855  
 Qy 427 AAGGGAATGCGCAGGTTGCGCAAGATCTCGCAGCTGATCAAAATTAAGCTGCTTAAGGCT 486  
 Db 856 AAGCAAGTGCCTGCTTCTCGAGCTGGCGCGGAGGACGATCGCCTCTCTGAGGCA 915  
 Qy 487 TGCTCAAGTGAAGTAAATGATGCTCCGAGTCCGCGCAGATACGATGCGGCTCTCAGACAGT 546  
 Db 916 TCCACTATCGAGATCATGCTCTAGAGACAGCCAGGCGCTACAAACCAAGACAGAGTGT 975  
 Qy 547 GTTCTGTTGGCGAACAACCAAGCTGACTCGCGCAGCAACTACCGCAAGGCTGGCAT---G 603  
 Db 976 ATCACTTCTTGAAGGACTTTCACCTACAGCAAGGACGACTTCCACCGTGCAGGCTGCAG 1035  
 Qy 604 GCCTACGTCATCGAGGATCTACTGCACCTTCTGCGGCTGCTACTCTATGCGCTGGAC 663  
 Db 1036 GTGGAGTTCATCAACCCCATCTTCGAGTTCGCGGCGCATGCGGCGCTGGGCTGGAC 1095  
 Qy 664 AACTCCATTAACGCGCTGCTCAGCGCTGTGCTCATCTTTT---CTGACCGCGCCAGGGTTG 720  
 Db 1096 GACGCTGAGTACGCGCTGCTCATGCCATCAACATCTTCTCGGCGCAGCGGCCCAACGCTG 1155  
 Qy 721 GAGCAGCGCAACTGCTGGAGAAATCCAGCGCTACTACCTGGAATACGCTCGCATCTAT 780  
 Db 1156 CAGGAGCGCGCGCTGCTGAGGCGTTGAGCAGCCCTACGTTGGAGGCGCTCTGTCTTAC 1215  
 Qy 781 ATCTGAAACACAGCTGAGCGGCTGCGGCTGCTGCTCATATACGCGCAAGATCTCTCA 840  
 Db 1216 ACGCGCATCAAGA-----GCGCGAGACAGCTGCGCTTCCGCGCATGCTCATG 1266  
 Qy 841 ATCTCTCTGAGCTACGACGCTCGCATGCAAACTCCAAATCTGATGTCATCTCCCTCAAG 900  
 Db 1267 AAGCTGTGAGCTGCGCAGCTGAGCTCTGTGCACTCGGAGCAGGTTCTTCGCTTGGCG 1326  
 Qy 901 CTCGAAGACAGAAAGCTGCGGCTTCTTCTCGAGGAGATCTGGGATGT 947  
 Db 1327 CTCGAGCAAGAAAGCTGCGGCTTCTGCTGTGAGATCTGGGACGT 1373  
 RESULT 7  
 US-11-136-527-2980  
 ; Sequence 2980, Application US/11136527  
 ; Publication No. US20050287570A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
 ; FILE REFERENCE: 031896-041000 (AM101086)  
 ; CURRENT APPLICATION NUMBER: US/11/136,527  
 ; CURRENT FILING DATE: 2005-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/574,294  
 ; PRIOR FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 362830  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 2980  
 ; LENGTH: 1959  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1899)..(1899)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 US-11-136-527-2980

Query Match 11.9%; Score 125.4; DB 8; Length 1959;  
 Best Local Similarity 46.7%; Pred. No. 2.3e-25;  
 Matches 364; Conservative 49; Mismatches 348; Indels 18; Gaps 4;

Qy	207	CCGCGAAGAAAACATCCCCAGTTTGA	CAGCCAAACAGCAGTTCTTATCGCCAGGCTCAT	266
Db	837	CGGGGAAGGAGAGGGGCATCCAGCTGA	CACGCGGCTCAGCAGCTGATGATCAACAGTTAGT	896
Qy	267	CTGGTACAGGACGGGTACGAGCAGCTTCT	GATGAAGATTTGAGAGGATTAACGACAG	326
Db	897	TGCGGCGAGCTGCAGTGCACAAAGCGATCTT	CTCCGACAGCCTTAAGTCACGCGCTG	956
Qy	327	GTGGCAGCAAGCGGACGATGAAACGAAGAGTCT	---GACACTCCCTTCGCGCAGATCCAC	383
Db	957	GCCCTTGGGTGCAGCCSKWASRMSSGAGACGCT	CGKASSRSGCTTTGCCCACTTCAC	1016
Qy	384	AGAGATGACTATCTCTACGGTCCAACTTAT	TGTTGAGAGTTTCGCGAAGGATTCGCAAGGTTT	443
Db	1017	TGAGCTAGCCATCATCTCAGTCCAGGAGATCGT	TGSACTTCGCCAAGCAGGTSCCAGGGTT	1076
Qy	444	CGCCAAGATCTCGCAGCGCTGATCAAAATTA	CGCTGCTTTAAGGCTTGCTCAAGTGAGGTAAT	503
Db	1077	CYTGCAGCTGSGCGGRAGGACCAAGATCGCC	STCMKQWASRMKCCACCATCGAGATCWT	1136
Qy	504	GATGCTCCGAGTCGCGCGACGATACGATCGG	CGCTCAGACAGTGTCTGTTTCGGCAACAA	563
Db	1137	GTGCTAGAGACAGCCAGACGTMTCACACCA	CGACGACGATGTCATCAGTTCTGTAAGGA	1196
Qy	564	CCAAAGCTATACCTCGGACAACTACCCAAAG	GCTGGCATG---GCCTACGTTCACGAGGA	620
Db	1197	CTTCACYTACAGCWAGGACGACTTCCACCGT	GCAGGCTTGACAGTGCAGTTCATCAATCC	1256
Qy	621	TCTACTGCATTTCTGCGGGTGCATGTACTCT	ATGCGTTCGGAACAACATCCATTACGGCT	680
Db	1257	CATCTWTGAGTTCTCTCGGGCTATGCGTTC	CGGCTGGGCTAGACATGACAGTATGCGCTT	1316
Qy	681	GCTCAAGGCTGTGCTCATCTTTTC---TGAC	CGGCGCAGGGTTGGACAGCGCGCAACTGGT	737
Db	1317	GCTCATTTGCCATCAACATATWTCTCAGHGG	ACCGGCBKMWKGGGAGGCCACCGTGT	1376
Qy	738	GGAAAGAAATCCAGCGGTACTACTGAAATAC	GTCTCCGCTATATATCTGTAACCAAGCTGAG	797
Db	1377	GGMGGCTWTGWSYAGMMWTATGTGGAKGCC	CTCKSKCCTRCASGARKATCRAGCDKCM	1436
Qy	798	CGGGTCGGCGGTTTCGTCCGTCATATACGG	CAAGATCTCTCANTCTCTGAGCTACG	857
Db	1437	GSRVASACSMKTCGCGCTTCCACGAAATGYT	CATGAAGCTGGTGAGC-----CTGCK	1487
Qy	858	CACGCTCGGCATGCAAAATCCAACTATGTGC	ATCTCCCTCAAGCTCAAGAACAGAAAGCT	917
Db	1488	CACCTCAGCTCCGTGCACTCGWGCAGGTTTTC	GCATTTGCGATGCGTCTCCAGGACAGAGCT	1547
Qy	918	GCCGCTTTCTCGAGGAGATCTCGGATGTGG	AGGACATGTCGCACACCCAACCGCCGC	976
Db	1548	GCCGCTTTGTGTCGAGATCTCGGATGTGCA	TGATGTAGGGGCGGCACAAGTGCCCTC	1606

## RESULT 8

US-11-166-412-18

; Sequence 18, Application US/11166412

; Publication No. US20060014231A1

**GENERAL INFORMATION:**

APPLICANT: Van Rompaey, Luc

APPLICANT: Tomme, Peter H.

**TITLE OF INVENTION: Methods and Compositions To Promote Bone Homeostasis**

FILE REFERENCE: P27,927-D USA

; CURRENT APPLICATION NUMBER: US/11/166,412

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PRIOR APPLICATION NUMBER: 60/582,704

;  
PRIOR FILING DATE: 2004-06-24

;  
PRIOR APPLICATION NUMBER: 60/630,449

PRIOR FILING DATE: 2004-11-23

PRIOR APPLICATION NUMBER: 60/6

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; SEQ ID NO 18
; LENGTH: 2033
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-166-412-18

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Query Match

367	Qy	CCCTTCGCGCAGATACAGAGATGAATATCTCTCA CGGTCCAACTTATCGTGGAGTTGCGG	426
1054	Db	CGCTTTTGCCACATTCA CGGAGCTGGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCT	1113
427	Qy	AAGGGATTGCGGGTTGCGCAAGATCTCGCAGCTGATCAAAATTACGTCGCTTAAAGGCT	486
1114	Db	AAGCAAGTGCCTGGTTTCTGCGAGCTGGGCGGGAGGACCAGATCGCCCTCTCTGAAAGGCA	1173
487	Qy	TGCTCAAGTGAGGTAATGATGCTCCGAGTCCGCGCAGATACGATCGGCGCTCAGACAGT	546
1174	Db	TCCACTATCGAGATCATGCTCTAGAGACAGCCAGCGGCTAACCAACGAGACAGAGTGT	1233
547	Qy	GTTCTGTTGCGCAACCAAGCGTACATCGCGGCAACAATACGCAAGGCTGGCAT--GG	603
1234	Db	ATCACCTTCTTGAAGGACTTTCACCTACAGCAAGGACGACTTCCACCGTGCAGGCTGCAG	1293
604	Qy	GCCTACGTCAATCAGGATCTACTGCATCTTCGCGGTGCAATGTACTCTATGGCGTTGGAC	663
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664	Qy	AACATCCATTACCGCGTGTCA CGGCTGTGCTCATCTTTT---CTGACCGGCGCAGGGTTG	720
1354	Db	GACGCTGAGTACGCCCTGCTCATCGCCATCAACATCTTCTCGGCGGACCGGCCCAACGTG	1413
721	Qy	GAGCAGCGCAACTGTGTGAAGAAATCCAGCGGTATCTACGTGAATACGCTCCGCATCTAT	780
1414	Db	CAGGAGCCGGCGCGGTGAGGGGTTGCAGCAGCCCTTACGTGGAGGCGCTGCTGTCTCTAC	1473
781	Qy	ATCTGAACACAGCTGAGCGGTCGGGCGGTTTCGTCGTCATATACGGCAAGATCCCTCA	840
1474	Db	ACGGGCATCAAGA-----GGCGCGAGGACAGCTGGCGCTCCGCGGCATGCTCATG	1524
841	Qy	ATCCTCTCTGAGCTAGCAGCTCGGCATGCAAAACTTCCAAACATGTGTCATCTCCCTCAAG	900
1525	Db	AAGCTGTGAGCTGCGCAGCTGAGCTCTGTGCACTCGGAGCAGGCTCTTCGCTTGGCGG	1584
901	Qy	CTCAAGAACAGAAAGCTGCCGCTTTCTCGAGGAGATCTGGAGTGT	947
1585	Db	CTCAGACACAGAAAGCTGCCGCTCTGCTCGGAGATCTGGACGT	1631

## RESULT 9

US-11-076-163-2

; Sequence 2, Application US/11076163

Publication No. US20050261319A1

**GENERAL INFORMATION:**

APPLICANT: Deuschle, Ulrich

APPLICANT: Loebbert, Ralph

APPLICANT: Blume, Beatrix

APPLICANT: Koegl, Manfred

APPLICANT: Kremoser, Claus

APPLICANT: Kober, Ingo

APPLICANT: Bauer, Ulrike

**APPLICANT: Hermann, Kristin**

APPLICANT: Albers, Michael

**TITLE OF INVENTION: Novel 2-**

**TITLE OF INVENTION:** LXR Nuc

; TITLE OF INVENTION: Property

FILE REFERENCE: BB-139

; CURRENT APPLICATION NUMBER: US/11/076,163

; CURRENT FILING DATE: 2005-03-09

; PRIOR APPLICATION NUMBER: PCT/BP03/10036



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QY 926 TCCTCGAGGAGATCTGGGATGTGGCGGA 953
Db 1348 TGCTCTCTGAGATCTGGGATGTGGCAGCA 1375

RESULT 11
US-11-136-527-2936
; Sequence 2936, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2936
; LENGTH: 2156
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2936

Query Match 7.2%; Score 75.8; DB 8; Length 2156;
Best Local Similarity 49.4%; Pred. No. 2.2e-11;
Matches 222; Conservative 1; Mismatches 223; Indels 3; Gaps 1;

QY 375 CCAGATCACAGAGATGACTATCTCCACGGTCCAACTTATTCGTGGAGTTTCGCGAGGGATT 434
Db 909 CAAGTTCAAGTGAATCTTCCACCAAGTGATATCAKARGACTGTGGAGTTTCGCCAAGAGCT 968
QY 435 GCCAGGGTTCCCAAGATCTCGCAGCCTGATCAAAATTACGCTTGTAAAGCTTGTCTCAAG 494
Db 969 TCCGGGCTTCAACACCTCACCATTGCGACAGATTACCTTTCTCAAGGCTGCCTGCCT 1028
QY 495 TGAGTTAATGATCTCGAGTCTGGGCGACATAGGATGGCGCTCAGACAGTTCTTGTT 554
Db 1029 GGACATCCTGATTTCTGGAAATCTGCACGCGGTACACACCTTGAGCAAGACACAATGACCTT 1088
QY 555 CGCGAACCAACGCGTACACTCGGACAACTACCGCAAGCTGGCATGCGCTACGTCAT 614
Db 1089 CTGATGGAGTACCTCGGACCGGACTGAGATGCAACAGCTGTGGCCCTCCAC 1148
QY 615 CGAGGATCTACTGACCTTCTGCGGTGTCATGTACTTATGGCGTTGGACAACTCCATTA 674
Db 1149 CGACTTGGTCTTTGGCTTGGCCAAACAGCTGTGCTGCCCTGGAGATGGACGATGCTGAGAC 1208
QY 675 CGCGTGTCTACGGCTGT----CGTCATCTTTTCGACCGGCCAGGGTTGGAGCAGCGGCA 731
Db 1209 CGGACTGCTCAGTGCCATCTGCTCCTCATCTGTGGAGACCGACAGGACCTGGAGCAGCCGA 1268
QY 732 ACTGGTGGAAAGAAATCAGCGGTACTACCTGAAATAGGCTCGCATCTATATCTCTGAACCA 791
Db 1269 CAAGGTGCAATGCTGACGAGCGCGTGTGGAGCACTGAAAGTCTATGTTCGGAACG 1328
QY 792 GCTGAGCGGTTCGGCGGTTGTCCTCGTCA 820
Db 1329 GAGGCCGAGCRRCCCCACATGTTCCCA 1357

RESULT 12
US-11-136-527-1966
; Sequence 1966, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527

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; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1966
; LENGTH: 2329
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1966

Query Match 7.0%; Score 74; DB 8; Length 2329;
Best Local Similarity 50.5%; Pred. No. 7.4e-11;
Matches 195; Conservative 4; Mismatches 184; Indels 3; Gaps 1;

QY 413 TCGTGAGTTTCGGAAGGATTGCCAGGTTTCGCAAGATCTCGCAGCCTGATCAAAATTA 472
Db 1532 TGGTAGAATTTGCCAAACAGATCCCGGCTTCCGTGACCTTTCTCAGCAGCAGCAGGTGA 1591
QY 473 CGCTGCTTAAAGCTTGTCTCAAGTGAGGTAATGATGCTCCGAGTTCGCGCGACGATACGATG 532
Db 1592 CCCTGCTTAAAGCTTGGCACCCTTTGAGGTGCTGATGTTGGCTTTCGCTCAATGTTCAACG 1651
QY 533 CGGCCTCAGACAGATGTTCTGTTTCGCGAACAACCAAGCGTACACTCGCGACAACTACGCA 592
Db 1652 TGAGGACACAGACAGATGTTCTCTGAGCGCGACAACTCAGCCTGCGAGGAGTCCGGTG 1711
QY 593 AGGCTGGCATGGCTTACGTCACTCGAGGATCTACTGCACCTTCTGCCGGTGCATGTACTTA 652
Db 1712 CCATGGCATGGTGGACCTGCTCAATGCCATGTTTGACWTGAGGAGAGCTCAACTCTIS 1771
QY 653 TGGCGTTGGACAAACATCCATTAAGCGCTGCTCAGCGCTGCTG---TCATCTTTTCTGACC 709
Db 1772 TGGCGTTTACTGAGGAGGAGCTGGGCTTTTTCAGCGCAGTGGTACTTGTCTCTGCAGASS 1831
QY 710 GGCACGGTTTGGAGCAGCGCAACTGTTGGAGAAATCCAGCGGTACTACCTGAATACGC 769
Db 1832 GCTCGGAAATGAGAAATTCGGCTTGGTGAGCAGCTCAGGAGACGCTGCTGGGGGCTC 1891
QY 770 TCGCATCTATATCTCTGAACCCAGCTG 795
Db 1892 TTCGGGCTCTGTTGCTGAAGACCG 1917

RESULT 13
US-11-112-908-15
; Sequence 15, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-15

Query Match 6.4%; Score 67.6; DB 8; Length 2355;
Best Local Similarity 50.3%; Pred. No. 4.7e-09;

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QY 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACCTGAATAGCTCCGCATCTAT 780
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Db 1135 CAGGACGAGCTCCAAGTAGRGRGACTGCAACACACATWGTGGAGGCCCTGCATGCCCKWK 1194
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 781 ATCCTGAACCAAGCTGAGCGGTCGGCGGTTGCTCGGTCAATATACGCGCAAGATCCTCTCA 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1195 GTVTCATCAACCAACCCCAAGACCGAY-----TGATGTTCCACGGATGYTAATG 1245
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 841 ATCCTCTCTGAGCTACGACGCTCGGCATGCAAAACTCCAAACATGTGCATCTCCCTCAAG 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1246 AAGYTGGTGAAGCTCCGGACTTTGAGCAGCGTCCCATTCAGAGCAAGTGTTCACCTTCGC 1305
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 901 CTCAGAACAGAAAGCTGCCGCTTTCTCGAGGAGATCTGGGATGTGGCGGA 953
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1306 CTCAGAGCAAAAAMTTCCCTTGTCTTCCGAGATYGGGATGTCCMCGA 1358
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Search completed: January 31, 2006, 16:57:42  
Job time : 402 secs





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181 CTCTCCGCAAGCTGTTGGAGACAAACCGGAGAAAAACATCCCGAGTTGACAGCAAC 240
181 CTCTCCGCAAGCTGTTGGAGACAAACCGGAGAAAAACATCCCGAGTTGACAGCAAC 240
241 CAGCAGTTCCTTATCCGCAAGCTCATCTGGTACGAGCGGGTACGAGCGCTTCTGAT 300
241 CAGCAGTTCCTTATCCGCAAGCTCATCTGGTACGAGCGGGTACGAGCGCTTCTGAT 300
301 GAAGATTGGAAGAGATTACGAGACGTGGCAGCAAGCGGAGCAAGTGAAGAGTCT 360
301 GAAGATTGGAAGAGATTACGAGACGTGGCAGCAAGCGGAGCAAGTGAAGAGTCT 360
361 GACATCCCTTCGCGCAGATCACAGATGACTATCTCAGCGTCCCACTTATCGTGGAG 420
361 GACATCCCTTCGCGCAGATCACAGATGACTATCTCAGCGTCCCACTTATCGTGGAG 420
421 TTCCGGAAGGAGTTGCGCAAGGTTGCGCAAGATCTCGCAGCTGATCAAAATAGCGTCT 480
421 TTCCGGAAGGAGTTGCGCAAGGTTGCGCAAGATCTCGCAGCTGATCAAAATAGCGTCT 480
481 AAGCTTGTCTCAAGTGAAGTAAATGATGCTCGAGTCCGCGAGATGAGATGCGGCTCA 540
481 AAGCTTGTCTCAAGTGAAGTAAATGATGCTCGAGTCCGCGAGATGAGATGCGGCTCA 540
541 GACAGTGTCTGTTCCGCAACCAAGCGTACACTCGCGCAACTACCGCAAGGCTGGC 600
541 GACAGTGTCTGTTCCGCAACCAAGCGTACACTCGCGCAACTACCGCAAGGCTGGC 600
601 ATGCGCTACGTCTACGAGGATCTACTGCACTTCTCGCGGTGCAATGATCTATGGCGTTG 660
601 ATGCGCTACGTCTACGAGGATCTACTGCACTTCTCGCGGTGCAATGATCTATGGCGTTG 660
661 GACAGATCCATTAAGCGTGTCTCAGCGGTGTGTGATCTTTCTGACCGCGCGGTTG 720
661 GACAGATCCATTAAGCGTGTCTCAGCGGTGTGTGATCTTTCTGACCGCGCGGTTG 720
721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTGATGATGATGATGATGATGAT 780
721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTGATGATGATGATGATGATGAT 780
781 ATCTCTGAAACCAAGCTGAGCGGTGCGCGCTTCTCGTCTATATACGCGCAAGTCTCTCA 840
781 ATCTCTGAAACCAAGCTGAGCGGTGCGCGCTTCTCGTCTATATACGCGCAAGTCTCTCA 840
841 ATCTCTCTGAGCTACGCAAGCTCGGAGTGCMAAACTCCCAACATGTCATCTCTCAAG 900
841 ATCTCTCTGAGCTACGCAAGCTCGGAGTGCMAAACTCCCAACATGTCATCTCTCAAG 900
901 CTCAAGAACAGAAAGCTGCGCGCTTCTCTGAGGAGATCTGGGATGCGGAGATGTCG 960
901 CTCAAGAACAGAAAGCTGCGCGCTTCTCTGAGGAGATCTGGGATGCGGAGATGTCG 960
961 CACACCCAAACCGCGCTTATCTCTGAGTCCCGCAAGATCTCTAGCGCTTCTGCGGACGC 1020
961 CACACCCAAACCGCGCTTATCTCTGAGTCCCGCAAGATCTCTAGCGCTTCTGCGGACGC 1020
1021 ATGCGGAGTCCGCGTTCGCGCGCTGCTCTGA 1054
1021 ATGCGGAGTCCGCGTTCGCGCGCTGCTCTGA 1054

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RESULT 2  
 US-10-239-134-3  
 ; Sequence 3, Application US/10239134  
 ; Publication No. US20040033600A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rohm and Haas Company  
 ; APPLICANT: Palli, Subba Reddy  
 ; APPLICANT: Kapitekaya, Marianna Zinovjevna  
 ; APPLICANT: Cress, Dean Ervin  
 ; TITLE OF INVENTION: No. US20040033600A1el Ecdysone Receptor-Based Inducible Gene Expr  
 ; FILE REFERENCE: RH0020  
 ; CURRENT APPLICATION NUMBER: US/10/239,134

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; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1054
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20040033600A1el Sequence
US-10-239-134-3

Query Match 100.0%; Score 1054; DB 7; Length 1054;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGAGTGGTGTAGTACCCGAGACTCAGTGGCCATGAAAGCGGAAAGAGAAAGACAG 60
Db 1 CTTGAGTGGTGTAGTACCCGAGACTCAGTGGCCATGAAAGCGGAAAGAGAAAGACAG 60
Qy 61 AAGGAGAGAGACAAACTGCTCTCAGCAGCAGCGGTGGACGACCATGCGGCCATT 120
Db 61 AAGGAGAGAGACAAACTGCTCTCAGCAGCAGCGGTGGACGACCATGCGGCCATT 120
Qy 121 ATGCACTGTGAACCTCCACTCTCTGAAGCAGCAAGGATTCAGCAAGTGGTCCCAAGGTTT 180
Db 121 ATGCACTGTGAACCTCCACTCTCTGAAGCAGCAAGGATTCAGCAAGTGGTCCCAAGGTTT 180
Qy 181 CTCTCCGCAAGCTGTTGGAGACAAACCGGCGAGAAAAACATCCCGAGTTGACAGCAAC 240
Db 181 CTCTCCGCAAGCTGTTGGAGACAAACCGGCGAGAAAAACATCCCGAGTTGACAGCAAC 240
Qy 241 CAGCAGTTCCTTATCCGCAAGCTCATCTGGTACCGGAGCGGTGACGAGCGCTTCTGAT 300
Db 241 CAGCAGTTCCTTATCCGCAAGCTCATCTGGTACCGGAGCGGTGACGAGCGCTTCTGAT 300
Qy 301 GAAGATTGGAAGAGATTACGAGACGTGGCAGCAAGCGGAGCAAGTGAAGAGTCT 360
Db 301 GAAGATTGGAAGAGATTACGAGACGTGGCAGCAAGCGGAGCAAGTGAAGAGTCT 360
Qy 361 GACATCCCTTCGCGCAGATCACAGATGATCTCCTCAAGTGCATCTTATCGTGGAG 420
Db 361 GACATCCCTTCGCGCAGATCACAGATGATCTCCTCAAGTGCATCTTATCGTGGAG 420
Qy 421 TTCCGGAAGGAGTTGCGCAAGGTTGCGCAAGATCTCGCAGCTGATCAAAATAGCGTCT 480
Db 421 TTCCGGAAGGAGTTGCGCAAGGTTGCGCAAGATCTCGCAGCTGATCAAAATAGCGTCT 480
Qy 481 AAGCTTGTCTCAAGTGAAGTAAATGATGCTCGAGTCCGCGAGATGAGATGCGGCTCA 540
Db 481 AAGCTTGTCTCAAGTGAAGTAAATGATGCTCGAGTCCGCGAGATGAGATGCGGCTCA 540
Qy 541 GACAGTGTCTGTTCCGCAACCAAGCGTACACTCGCGCAACTACCGCAAGGCTGGC 600
Db 541 GACAGTGTCTGTTCCGCAACCAAGCGTACACTCGCGCAACTACCGCAAGGCTGGC 600
Qy 601 ATGCGCTACGTCTACGAGGATCTACTGCACTTCTCGCGGTGCAATGATCTATGGCGTTG 660
Db 601 ATGCGCTACGTCTACGAGGATCTACTGCACTTCTCGCGGTGCAATGATCTATGGCGTTG 660
Qy 661 GACAGATCCATTAAGCGTGTCTCAGCGGTGTGTGATCTTTCTGACCGCGCGGTTG 720
Db 661 GACAGATCCATTAAGCGTGTCTCAGCGGTGTGTGATCTTTCTGACCGCGCGGTTG 720
Qy 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTGATGATGATGATGATGATGAT 780
Db 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTGATGATGATGATGATGATGAT 780
Qy 781 ATCTCTGAAACCAAGCTGAGCGGTGCGCGCTTCTCGTCTATATACGCGCAAGTCTCTCA 840

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Db 781 ATCTGAAACAGCTGAGCGGTGCGGTTGCTGCGTCATATACGGCAAGATCTCTCA 840  
Qy 841 ATCTCTCTGAGCTACGACGCTCGGATGCAAAATCTCAACATGTGATCTCCTCAAG 900  
Db 841 ATCTCTCTGAGCTACGACGCTCGGATGCAAAATCTCAACATGTGATCTCCTCAAG 900  
Qy 901 CTCAAGAACAGAAAGCTGCGGCTTTCTCGAGAGATCTGGATGTGGCGGACATGTG 960  
Db 901 CTCAAGAACAGAAAGCTGCGGCTTTCTCGAGAGATCTGGATGTGGCGGACATGTG 960  
Qy 961 CACACCAACCGCGCTATCTCGAGTCCGCCACGATCTAGCCCTCGCGGACGC 1020  
Db 961 CACACCAACCGCGCTATCTCGAGTCCGCCACGATCTAGCCCTCGCGGACGC 1020  
Qy 1021 ATCCCGATGCGGCTCGGCGGCTGCTCTGA 1054  
Db 1021 ATCCCGATGCGGCTCGGCGGCTGCTCTGA 1054  
RESULT 3  
US-10-468-199-65  
; Sequence 65, Application US/10468199  
; Publication No. US20040096942A1  
; GENERAL INFORMATION:  
; APPLICANT: Palli, Subba R.  
; APPLICANT: Kapitekaya, Marianna Z.  
; TITLE OF INVENTION: Chimeric retinoid X receptors and their use in a novel ecdysone  
; TITLE OF INVENTION: receptor-based inducible gene expression system  
; FILE REFERENCE: A01238-US  
; CURRENT APPLICATION NUMBER: US/10/468,199  
; CURRENT FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/294,819  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: PCT/US02/05706  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 65  
; LENGTH: 1054  
; TYPE: DNA  
; ORGANISM: Choristoneura fumiferana  
US-10-468-199-65  
Query Match 100.0%; Score 1054; DB 7; Length 1054;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCTGAGTGGCTAGTACCGGACTCAGTGGCCCATGAAGCGGAAAGAGAAAGCAAG 60  
Db 1 CCTGAGTGGCTAGTACCGGACTCAGTGGCCCATGAAGCGGAAAGAGAAAGCAAG 60  
Qy 61 AAGGAGAGGACAACTGCTGTGACGACGAGCGGTGGAGCACCACATGCCGCCATT 120  
Db 61 AAGGAGAGGACAACTGCTGTGACGACGAGCGGTGGAGCACCACATGCCGCCATT 120  
Qy 121 ATGCAAGTGTGAACCTCCACTCTCTGAAGCAAGGATTCACGAAGTGTGCCAAGGTTT 180  
Db 121 ATGCAAGTGTGAACCTCCACTCTCTGAAGCAAGGATTCACGAAGTGTGCCAAGGTTT 180  
Qy 181 CTCTCCGACAAAGCTGTGGAGACAAACCGGAGAAAAATCATCCCGCTTGACAGCCAA 240  
Db 181 CTCTCCGACAAAGCTGTGGAGACAAACCGGAGAAAAATCATCCCGCTTGACAGCCAA 240  
Qy 241 CAGCAGTCTTATGCGCAGGCTCATCTGGTACAGGACGGGTACGAGCAGCCTTCTGAT 300  
Db 241 CAGCAGTCTTATGCGCAGGCTCATCTGGTACAGGACGGGTACGAGCAGCCTTCTGAT 300  
Qy 301 GAAGATTTGAAGAGATTTACGACAGCTGGCAGCAAGCGGACGATGAAGACGAAGATCT 360  
Db 301 GAAGATTTGAAGAGATTTACGACAGCTGGCAGCAAGCGGACGATGAAGACGAAGATCT 360  
Qy 361 GACACTCCCTTCGCCAGATCACAGAGATGATCTCTCACGGTCCAACTTATCGTGGAG 420

Db 361 GACACTCCCTTCGCCAGATCACAGAGATGATATCTCTCACGGTCCAACTTATCGTGGAG 420  
Qy 421 TTCCGGAAGGATTTCCAGGGTTCCCAAGATCTCGAGGCTGATCAAAATTTACGCTGCTT 480  
Db 421 TTCCGGAAGGATTTCCAGGGTTCCCAAGATCTCGAGGCTGATCAAAATTTACGCTGCTT 480  
Qy 481 AAGGCTTGTCTCAAGTGAAGTAATGATCTCCGAGTCCGGGACGATACGATGCGGCTCA 540  
Db 481 AAGGCTTGTCTCAAGTGAAGTAATGATCTCCGAGTCCGGGACGATACGATGCGGCTCA 540  
Qy 541 GACAGTGTCTGTTCCGGAACCAAGCGGTACACTCGGACCAACTACCGCAAGGCTGGC 600  
Db 541 GACAGTGTCTGTTCCGGAACCAAGCGGTACACTCGGACCAACTACCGCAAGGCTGGC 600  
Qy 601 ATGGCCTTACGTCATCGAGGATCTACTGCACCTTCTGCGGCTGATGTACTCTATGGCGTTG 660  
Db 601 ATGGCCTTACGTCATCGAGGATCTACTGCACCTTCTGCGGCTGATGTACTCTATGGCGTTG 660  
Qy 661 GACAAATCCATTACGCGCTGCTCACGCGTGTCTCATCTTTTCTGACCGGCTGCTGAT 720  
Db 661 GACAAATCCATTACGCGCTGCTCACGCGTGTCTCATCTTTTCTGACCGGCTGCTGAT 720  
Qy 721 GAGCGCGCGCACTGTTGGAGAAATCCAGCGGTACTACCTGAATACGCTCGCATCTAT 780  
Db 721 GAGCGCGCGCACTGTTGGAGAAATCCAGCGGTACTACCTGAATACGCTCGCATCTAT 780  
Qy 781 ATCTGAAACAGCTGAGCGGTGCGGCTGCTGCTGCTCATATACGGCAAGATCTCTCA 840  
Db 781 ATCTGAAACAGCTGAGCGGTGCGGCTGCTGCTGCTCATATACGGCAAGATCTCTCA 840  
Qy 841 ATCTCTCTGAGCTACGACGCTCGGATGCAAAACTCCCAACATGTGCTCTCCCTCAAG 900  
Db 841 ATCTCTCTGAGCTACGACGCTCGGATGCAAAACTCCCAACATGTGCTCTCCCTCAAG 900  
Qy 901 CTCAAGAACAGAAAGCTGCGGCTTTCTCGAGGAGATCTGGGATGTGGCGGACATGTG 960  
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Qy 961 CACACCAACCGCGCTATCTCTCGAGTCCGCCACGATCTCTAGCCCTCGCGGACGC 1020  
Db 961 CACACCAACCGCGCTATCTCTCGAGTCCGCCACGATCTCTAGCCCTCGCGGACGC 1020  
Qy 1021 ATCCCGATGCGGCTCGGCGGCTGCTCTGA 1054  
Db 1021 ATCCCGATGCGGCTCGGCGGCTGCTCTGA 1054  
RESULT 4  
US-10-783-810-1  
; Sequence 1, Application US/10783810  
; Publication No. US20040171651A1  
; GENERAL INFORMATION:  
; APPLICANT: Hornmann, Robert E  
; APPLICANT: Chortyk, Orestes  
; APPLICANT: Le, Dat Phat  
; TITLE OF INVENTION: Oxadiazoline ligands for modulating the expression of exogenous  
; FILE REFERENCE: A01494-US  
; CURRENT APPLICATION NUMBER: US/10/783,810  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US 60/449,467  
; PRIOR FILING DATE: 2003-02-21  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1054  
; TYPE: DNA  
; ORGANISM: Choristoneura fumiferana  
US-10-783-810-1  
Query Match 100.0%; Score 1054; DB 7; Length 1054;  
Best Local Similarity 100.0%; Pred. No. 0;

		Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	CTGTAGTGGT	AGTACCGGAG	CTCAGTGG	CCCATG	AGCGGAA	AGAGAA	AGCAG	60		
Db	1	CTGTAGTGGT	AGTACCGGAG	CTCAGTGG	CCCATG	AGCGGAA	AGAGAA	AGCAG	60		
Qy	61	AAGGAGAGG	CAAACTGC	CTGTG	CAGCAG	CAGCAG	CGGTG	GACG	120		
Db	61	AAGGAGAGG	CAAACTGC	CTGTG	CAGCAG	CAGCAG	CGGTG	GACG	120		
Qy	121	ATGCACTG	GAAGTAA	CTCCAC	CTCTG	GAAGCAG	CAAGGAT	TCAG	180		
Db	121	ATGCACTG	GAAGTAA	CTCCAC	CTCTG	GAAGCAG	CAAGGAT	TCAG	180		
Qy	181	CTCTCCG	ACAGCTGT	GGAGCA	AAACCCG	CAGAAAA	CATCC	CCGAGT	240		
Db	181	CTCTCCG	ACAGCTGT	GGAGCA	AAACCCG	CAGAAAA	CATCC	CCGAGT	240		
Qy	241	CAGCAGT	TCCTTAT	CGCCAG	CTCAT	CTGTG	TACG	AGCG	300		
Db	241	CAGCAGT	TCCTTAT	CGCCAG	CTCAT	CTGTG	TACG	AGCG	300		
Qy	301	GAAGATT	TGAAGAG	ATTAC	CGCAG	AGTAC	CGGAG	CGGAG	360		
Db	301	GAAGATT	TGAAGAG	ATTAC	CGCAG	AGTAC	CGGAG	CGGAG	360		
Qy	361	GACACTC	CTCTG	CGGAG	ATCA	CAGAG	ATGACT	TCTC	420		
Db	361	GACACTC	CTCTG	CGGAG	ATCA	CAGAG	ATGACT	TCTC	420		
Qy	421	TTCCG	CAAGGAT	TGCGCAG	GTTCG	CAAGT	CTCG	CAGC	480		
Db	421	TTCCG	CAAGGAT	TGCGCAG	GTTCG	CAAGT	CTCG	CAGC	480		
Qy	481	AAGGCTT	GTCTCA	AGTGA	GTATG	ATGCT	CCGAG	TGCG	540		
Db	481	AAGGCTT	GTCTCA	AGTGA	GTATG	ATGCT	CCGAG	TGCG	540		
Qy	541	GACAGT	GTCTG	TTCCG	CAAA	CAAC	CAAG	CGGT	600		
Db	541	GACAGT	GTCTG	TTCCG	CAAA	CAAC	CAAG	CGGT	600		
Qy	601	ATGCG	CTAC	GTG	CTG	CTG	CTG	CTG	660		
Db	601	ATGCG	CTAC	GTG	CTG	CTG	CTG	CTG	660		
Qy	661	GACAA	CTC	ATTA	CGCG	CTG	CTG	CTG	720		
Db	661	GACAA	CTC	ATTA	CGCG	CTG	CTG	CTG	720		
Qy	721	GAGCAG	CGCA	CTGTG	GGAGAA	ATCC	AGCG	GTAT	780		
Db	721	GAGCAG	CGCA	CTGTG	GGAGAA	ATCC	AGCG	GTAT	780		
Qy	781	ATCTG	AAAC	CAAG	CTG	CGG	CTG	CTG	840		
Db	781	ATCTG	AAAC	CAAG	CTG	CGG	CTG	CTG	840		
Qy	841	ATCTCT	CTG	AGCT	TAC	CGC	ATG	CAAA	900		
Db	841	ATCTCT	CTG	AGCT	TAC	CGC	ATG	CAAA	900		
Qy	901	CTCAG	AAAC	CAAG	CTG	CGG	CTG	CTG	960		
Db	901	CTCAG	AAAC	CAAG	CTG	CGG	CTG	CTG	960		
Qy	961	CACAC	CAAC	CGCG	CTAT	CTCT	CGAG	TGCG	1020		
Db	961	CACAC	CAAC	CGCG	CTAT	CTCT	CGAG	TGCG	1020		
Qy	1021	ATCGC	CAAT	CGCG	CTG	CGG	CTG	CTG	1054		
Db	1021	ATCGC	CAAT	CGCG	CTG	CGG	CTG	CTG	1054		

RESULT 5  
US-10-775-883-1  
; Sequence 1, Application US/10775883  
; Publication No. US20050209283A1  
; GENERAL INFORMATION:  
; APPLICANT: Hormann, Robert E  
; APPLICANT: Chortyk, Orestes  
; APPLICANT: Smith, Howard  
; APPLICANT: Meteyer, Thomas  
; APPLICANT: Tice, Colin M  
; TITLE OF INVENTION: DIACYLHYDRAZINE LIGANDS FOR MODULATING THE EXPRESSION OF  
; TITLE OF INVENTION: EXOGENOUS GENES IN MAMMALIAN SYSTEMS VIA AN RCDISONE RECEPTOR  
; FILE REFERENCE: A01381-US  
; CURRENT APPLICATION NUMBER: US/10/775,883  
; PRIOR FILING DATE: 2004-02-09  
; PRIOR APPLICATION NUMBER: US 60/446,233  
; PRIOR FILING DATE: 2003-02-10  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1054  
; TYPE: DNA  
; ORGANISM: Choriostoneura fumiferana  
; US-10-775-883-1

		Query Match 100.0%; Score 1054; DB 9; Length 1054; Best Local Similarity 100.0%; Pred. No. 0; Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	CTGTAGTGGT	AGTACCGGAG	CTCAGTGG	CCCATG	AGCGGAA	AGAGAA	AGCAG	60		
Db	1	CTGTAGTGGT	AGTACCGGAG	CTCAGTGG	CCCATG	AGCGGAA	AGAGAA	AGCAG	60		
Qy	61	AAGGAGAGG	CAAACTGC	CTGTG	CAGCAG	CAGCAG	CGGTG	GACG	120		
Db	61	AAGGAGAGG	CAAACTGC	CTGTG	CAGCAG	CAGCAG	CGGTG	GACG	120		
Qy	121	ATGCACTG	GAAGTAA	CTCCAC	CTCTG	GAAGCAG	CAAGGAT	TCAG	180		
Db	121	ATGCACTG	GAAGTAA	CTCCAC	CTCTG	GAAGCAG	CAAGGAT	TCAG	180		
Qy	181	CTCTCCG	ACAGCTGT	GGAGCA	AAACCCG	CAGAAAA	CATCC	CCGAGT	240		
Db	181	CTCTCCG	ACAGCTGT	GGAGCA	AAACCCG	CAGAAAA	CATCC	CCGAGT	240		
Qy	241	CAGCAGT	TCCTTAT	CGCCAG	CTCAT	CTGTG	TACG	AGCG	300		
Db	241	CAGCAGT	TCCTTAT	CGCCAG	CTCAT	CTGTG	TACG	AGCG	300		
Qy	301	GAAGATT	TGAAGAG	ATTAC	CGCAG	AGTAC	CGGAG	CGGAG	360		
Db	301	GAAGATT	TGAAGAG	ATTAC	CGCAG	AGTAC	CGGAG	CGGAG	360		
Qy	361	GACACTC	CTCTG	CGGAG	ATCA	CAGAG	ATGACT	TCTC	420		
Db	361	GACACTC	CTCTG	CGGAG	ATCA	CAGAG	ATGACT	TCTC	420		
Qy	421	TTCCG	CAAGGAT	TGCGCAG	GTTCG	CAAGT	CTCG	CAGC	480		
Db	421	TTCCG	CAAGGAT	TGCGCAG	GTTCG	CAAGT	CTCG	CAGC	480		
Qy	481	AAGGCTT	GTCTCA	AGTGA	GTATG	ATGCT	CCGAG	TGCG	540		
Db	481	AAGGCTT	GTCTCA	AGTGA	GTATG	ATGCT	CCGAG	TGCG	540		
Qy	541	GACAGT	GTCTG	TTCCG	CAAA	CAAC	CAAG	CGGT	600		
Db	541	GACAGT	GTCTG	TTCCG	CAAA	CAAC	CAAG	CGGT	600		
Qy	601	ATGCG	CTAC	GTG	CTG	CTG	CTG	CTG	660		
Db	601	ATGCG	CTAC	GTG	CTG	CTG	CTG	CTG	660		
Qy	661	GACAA	CTC	ATTA	CGCG	CTG	CTG	CTG	720		
Db	661	GACAA	CTC	ATTA	CGCG	CTG	CTG	CTG	720		
Qy	721	GAGCAG	CGCA	CTGTG	GGAGAA	ATCC	AGCG	GTAT	780		
Db	721	GAGCAG	CGCA	CTGTG	GGAGAA	ATCC	AGCG	GTAT	780		
Qy	781	ATCTG	AAAC	CAAG	CTG	CGG	CTG	CTG	840		
Db	781	ATCTG	AAAC	CAAG	CTG	CGG	CTG	CTG	840		
Qy	841	ATCTCT	CTG	AGCT	TAC	CGC	ATG	CAAA	900		
Db	841	ATCTCT	CTG	AGCT	TAC	CGC	ATG	CAAA	900		
Qy	901	CTCAG	AAAC	CAAG	CTG	CGG	CTG	CTG	960		
Db	901	CTCAG	AAAC	CAAG	CTG	CGG	CTG	CTG	960		
Qy	961	CACAC	CAAC	CGCG	CTAT	CTCT	CGAG	TGCG	1020		
Db	961	CACAC	CAAC	CGCG	CTAT	CTCT	CGAG	TGCG	1020		
Qy	1021	ATCGC	CAAT	CGCG	CTG	CGG	CTG	CTG	1054		
Db	1021	ATCGC	CAAT	CGCG	CTG	CGG	CTG	CTG	1054		



; APPLICANT: Kapitskaya, Marianna Zinovjevna  
 ; APPLICANT: Cress, Dean Ervin  
 ; TITLE OF INVENTION: No. US20040033600A1e1 Bcdysone Receptor-Based Inducible Gene Expression  
 ; FILE REFERENCE: RH0020  
 ; CURRENT APPLICATION NUMBER: US/10/239,134  
 ; PRIOR FILING DATE: 2002-09-19  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR FILING DATE: 2001-02-20  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1288  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: No. US20040033600A1e1 Sequence  
 ; US-10-239-134-1

Query Match 100.0%; Score 1054; DB 7; Length 1288;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTGTAGTGGTGTACCCGAGACTCAGTGGCCATGAGCGGAAAGAGAAAGCAG	60
Db	235	CTGTAGTGGTGTACCCGAGACTCAGTGGCCATGAGCGGAAAGAGAAAGCAG	294
Qy	61	AAGGAGAGGACAAATCGCTGTCAGCAGCAGCGGTGACGACCATGCGCCCAT	120
Db	295	AAGGAGAGGACAAATCGCTGTCAGCAGCAGCGGTGACGACCATGCGCCCAT	354
Qy	121	ATGCAGTGTGAACCTCCACTCTGAGCAGCAGGATTCAGCAAGTGTGCTCAAG	180
Db	355	ATGCAGTGTGAACCTCCACTCTGAGCAGCAGGATTCAGCAAGTGTGCTCAAG	414
Qy	181	CTCTCCGACAAAGCTGTGGAGCAAAACCGCGCAGAAAACATCCCCAGTTG	240
Db	415	CTCTCCGACAAAGCTGTGGAGCAAAACCGCGCAGAAAACATCCCCAGTTG	474
Qy	241	CAGCAGTGTCTTATCGCAGGCTCATCTGTCAGCAGCGGTACGAGCAGCTT	300
Db	475	CAGCAGTGTCTTATCGCAGGCTCATCTGTCAGCAGCGGTACGAGCAGCTT	534
Qy	301	GAAGATTTGAAGAGGATTAACGACAGCTGTCAGCAGCGGTACGAGCAGCT	360
Db	535	GAAGATTTGAAGAGGATTAACGACAGCTGTCAGCAGCGGTACGAGCAGCT	594
Qy	361	GACACTCCCTTCGCGCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCG	420
Db	595	GACACTCCCTTCGCGCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCG	654
Qy	421	TTCCGAAAGGATTTGCCAGGTTTCGCAAGATCTCGCAGCTCATCAAAATTA	480
Db	655	TTCCGAAAGGATTTGCCAGGTTTCGCAAGATCTCGCAGCTCATCAAAATTA	714
Qy	481	AAGCTTTGCTCAAGTGAAGGTAATGATCTCCGAGTCCGCGGACGATACGAT	540
Db	715	AAGCTTTGCTCAAGTGAAGGTAATGATCTCCGAGTCCGCGGACGATACGAT	774
Qy	541	GACAGTGTCTTGTTCGCGAAACAAACGAGGTACACTCGGACAACTACCGCA	600
Db	775	GACAGTGTCTTGTTCGCGAAACAAACGAGGTACACTCGGACAACTACCGCA	834
Qy	601	ATGCGCTACCTTCAGGAGTCTACTGCACTTCGCGGTGCAATGATCTATGG	660
Db	835	ATGCGCTACCTTCAGGAGTCTACTGCACTTCGCGGTGCAATGATCTATGG	894
Qy	661	GACAACTTCAACGCGCTGCTCAGCGGTGTGTCTATCTTTTTCGACCGCGG	720
Db	895	GACAACTTCAACGCGCTGCTCAGCGGTGTGTCTATCTTTTTCGACCGCGG	954

Qy	721	GAGCAGCCCAACTGTGTGAAGAAATCCAGCGGTACTACTGAATACGCTCCGATCTAT	780
Db	955	GAGCAGCCCAACTGTGTGAAGAAATCCAGCGGTACTACTGAATACGCTCCGATCTAT	1014
Qy	781	ATCCTGAAACAGCTGAGCGGTTCGGCGCTTCTCGTTCATATACGCGCAAGATCTCTCA	840
Db	1015	ATCCTGAAACAGCTGAGCGGTTCGGCGCTTCTCGTTCATATACGCGCAAGATCTCTCA	1074
Qy	841	ATCCTCTCTGAGCTACGACAGCTCGGCATGCAAAACTCCAAATGTCATCTCCCTCAAG	900
Db	1075	ATCCTCTCTGAGCTACGACAGCTCGGCATGCAAAACTCCAAATGTCATCTCCCTCAAG	1134
Qy	901	CTCAAGAACAGAAAGCTGCGCTTCTCTGAGGAGATCTGGGATGCGGACATGTCG	960
Db	1135	CTCAAGAACAGAAAGCTGCGCTTCTCTGAGGAGATCTGGGATGCGGACATGTCG	1194
Qy	961	CACACCAACCGCGCTTCTCTGAGTCCCGCAGCAATCTCTAGCCCTGCGCGCAGCG	1020
Db	1195	CACACCAACCGCGCTTCTCTGAGTCCCGCAGCAATCTCTAGCCCTGCGCGCAGCG	1254
Qy	1021	ATGCGCGATGCGCGCTGCGCGCGCTGCTCTGA	1054
Db	1255	ATGCGCGATGCGCGCTGCGCGCGCTGCTCTGA	1288

RESULT 8  
 US-10-468-199-59  
 ; Sequence 59, Application US/10468199  
 ; Publication No. US20040096942A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Palli, Subba R.  
 ; APPLICANT: Kapitskaya, Marianna Z.  
 ; TITLE OF INVENTION: Chimeric retinoid X receptors and their use in a novel ecdysone  
 ; FILE REFERENCE: receptor-based inducible gene expression system  
 ; CURRENT APPLICATION NUMBER: US/10/468,199  
 ; PRIOR FILING DATE: 2002-02-20  
 ; PRIOR FILING DATE: 2001-05-31  
 ; PRIOR FILING DATE: 2001-05-31  
 ; PRIOR FILING DATE: 2002-02-20  
 ; NUMBER OF SEQ ID NOS: 75  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 59  
 ; LENGTH: 1288  
 ; TYPE: DNA  
 ; ORGANISM: Choristoneura fumiferana  
 ; US-10-468-199-59

Query Match 100.0%; Score 1054; DB 7; Length 1288;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTGTAGTGGTGTACCCGAGACTCAGTGGCCATGAGCGGAAAGAGAAAGCAG	60
Db	235	CTGTAGTGGTGTACCCGAGACTCAGTGGCCATGAGCGGAAAGAGAAAGCAG	294
Qy	61	AAGGAGAGGACAAATCGCTGTCAGCAGCAGCGGTGACGACCATGCGCCCAT	120
Db	295	AAGGAGAGGACAAATCGCTGTCAGCAGCAGCGGTGACGACCATGCGCCCAT	354
Qy	121	ATGCAGTGTGAACCTCCACTCTGAGCAGCAGGATTCAGCAAGTGTGCTCAAG	180
Db	355	ATGCAGTGTGAACCTCCACTCTGAGCAGCAGGATTCAGCAAGTGTGCTCAAG	414
Qy	181	CTCTCCGACAAAGCTGTGGAGCAAAACCGCGCAGAAAACATCCCCAGTTG	240
Db	415	CTCTCCGACAAAGCTGTGGAGCAAAACCGCGCAGAAAACATCCCCAGTTG	474
Qy	241	CAGCAGTGTCTTATCGCAGGCTCATCTGTCAGCAGCGGTACGAGCAGCTT	300
Db	475	CAGCAGTGTCTTATCGCAGGCTCATCTGTCAGCAGCGGTACGAGCAGCTT	534

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Qy 301 GAAGATTGGAAGAGATTACGACAGCTGGGCGAGCAAGCGGACGATGAAACGAAGAGTCT 360
Db 535 GAAGATTGGAAGAGATTACGACAGCTGGGCGAGCAAGCGGACGATGAAACGAAGAGTCT 594
Qy 361 GACACTCCCTCCGCGAGATCAGAGATGACTATCTCAGGTCGAACCTATCGTGGAG 420
Db 595 GACACTCCCTCCGCGAGATCAGAGATGACTATCTCAGGTCGAACCTATCGTGGAG 654
Qy 421 TTCGCGAAGGATTGCGCAGGTTGCGCAAGATCTCGACGCTGATCAAAATACGCTGCTT 480
Db 655 TTCGCGAAGGATTGCGCAGGTTGCGCAAGATCTCGACGCTGATCAAAATACGCTGCTT 714
Qy 481 AAGGCTTGCTCAAGTGAAGTAAATGATCTCCGATCGCGGCGAGATGATGATGATGATGAT 540
Db 715 AAGGCTTGCTCAAGTGAAGTAAATGATCTCCGATCGCGGCGAGATGATGATGATGATGATGAT 774
Qy 541 GACAGTCTTCTGTTGCGGACCAACCAAGCGTACACTCGCGCAACTACCGCAAGGCTGGC 600
Db 775 GACAGTCTTCTGTTGCGGACCAACCAAGCGTACACTCGCGCAACTACCGCAAGGCTGGC 834
Qy 601 ATGGCTTACGTCATCGAGGATCTACTGCACTTCTGCGGCTGATGATCTATGCGGCTTG 660
Db 835 ATGGCTTACGTCATCGAGGATCTACTGCACTTCTGCGGCTGATGATCTATGCGGCTTG 894
Qy 661 GACAAATCCATTAAGCGCTGCTCAAGGCTGCTGATCTCTTTCTGACCGGCGAGGTTG 720
Db 895 GACAAATCCATTAAGCGCTGCTCAAGGCTGCTGATCTCTTTCTGACCGGCGAGGTTG 954
Qy 721 GAGCAGCGGCAACTGTTGGAAGAAATCCAGCGGTACTACCTGAATACGCTCGGATCTAT 780
Db 955 GAGCAGCGGCAACTGTTGGAAGAAATCCAGCGGTACTACCTGAATACGCTCGGATCTAT 1014
Qy 781 ATCTGAAACAGCTGAGCGGTCGCGGCTTCTGCGGCTGATGATGATGATGATGATGATGAT 840
Db 1015 ATCTGAAACAGCTGAGCGGTCGCGGCTTCTGCGGCTGATGATGATGATGATGATGATGAT 1074
Qy 841 ATCTCTCTGAGTACGACGCTCGGATGCAAAACTCCAACTGTCATCTCCCTCAAG 900
Db 1075 ATCTCTCTGAGTACGACGCTCGGATGCAAAACTCCAACTGTCATCTCCCTCAAG 1134
Qy 901 CTGAAGACAGAAAGCTGCGGCTTCTGCGGCTGATGATGATGATGATGATGATGATGATGAT 960
Db 1135 CTGAAGACAGAAAGCTGCGGCTTCTGCGGCTGATGATGATGATGATGATGATGATGATGAT 1194
Qy 961 CACACCAACCGCGCTTATCTCGAGTCCCGGCTGATGATGATGATGATGATGATGATGATGAT 1020
Db 1195 CACACCAACCGCGCTTATCTCGAGTCCCGGCTGATGATGATGATGATGATGATGATGATGAT 1254
Qy 1021 ATGCGGATGCGGCTCGGCGGCTGCTCTGA 1054
Db 1255 ATGCGGATGCGGCTCGGCGGCTGCTCTGA 1288
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RESULT 9  
US-09-965-697-4  
; Sequence 4, Application US/09965697  
; Patent No. US20020110861A1  
; GENERAL INFORMATION:  
; APPLICANT: Hormann, Robert E.  
; APPLICANT: Palli, Subba Reddy  
; APPLICANT: Carlson, Glenn R.  
; APPLICANT: Cress, Dean E.  
; APPLICANT: Dhadialla, Tarlochan S.  
; APPLICANT: Herzog, Ronald P.  
; APPLICANT: Kudia, Arthur J.  
; APPLICANT: Philip, Mohan  
; TITLE OF INVENTION: Multiple Inducible Gene Regulation System  
; FILE REFERENCE: RH-0036 (DN A01115A)  
; CURRENT APPLICATION NUMBER: US/09/965,697  
; PRIORITY FILING DATE: 2001-09-27  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 16

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; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 1290  
; TYPE: DNA  
; ORGANISM: Choristoneura fumiferana  
US-09-965-697-4  
  
Query Match 97.7%; Score 1029.4; DB 3; Length 1290;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1052; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
  
Qy 1 CCTGAGTGCCTAGTACCCGAGACTCAGTGCCTCCATGAGCGGAAAGAGAAAGCAAGCAG 60  
Db 237 CCTGAGTGCCTAGTACCCGAGACTCAGTGCCTCCATGAGCGGAAAGAGAAAGCAAGCAG 296  
Qy 61 AAGGAGAAAGCAAACTGCTGTGACGACGAGCGGTGACGACCAATGATGATGATGATGATGAT 120  
Db 297 AAGGAGAAAGCAAACTGCTGTGACGACGAGCGGTGACGACCAATGATGATGATGATGATGAT 356  
Qy 121 ATGCAAGTGTGAACCTCCACCTCTGAAAGCAGCAAGGATTCACGAAAGTGGTCCCAAGGTTT 180  
Db 357 ATGCAAGTGTGAACCTCCACCTCTGAAAGCAGCAAGGATTCACGAAAGTGGTCCCAAGGTTT 416  
Qy 181 CTCTCCGACAAAGCTGTTGAGAGCAAAACCGGCGAGAAACATCCGCCAGATTGACAGCCAAC 240  
Db 417 CTCTCCGACAAAGCTGTTGAGAGCAAAACCGGCGAGAAACATCCGCCAGATTGACAGCCAAC 476  
Qy 241 CAGCAGTTCCTTATTCGCGAGGCTCATCTGTGTACGAGACGGGTACGAGCAGCCTTCTGAT 300  
Db 477 CAGCAGTTCCTTATTCGCGAGGCTCATCTGTGTACGAGACGGGTACGAGCAGCCTTCTGAT 536  
Qy 301 GAAGATTGGAAGAGATTACGACAGCTGGGCGAGCAAGCGGACGATGAAACGAAGAGTCT 360  
Db 537 GAAGATTGGAAGAGATTACGACAGCTGGGCGAGCAAGCGGACGATGAAACGAAGAGTCT 596  
Qy 361 GACACTCCCTTCGCGAGATCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
Db 597 GACACTCCCTTCGCGAGATCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 656  
Qy 421 TTGCGAAGGAGTTCGCGAGGTTGCGGAGTTCGCGAGTTCGCGAGTTCGCGAGTTCGCGAGTTC 480  
Db 657 TTGCGAAGGAGTTCGCGAGGTTGCGGAGTTCGCGAGTTCGCGAGTTCGCGAGTTCGCGAGTTC 716  
Qy 481 AAGGCTTGCTCAAGTGAAGTAAATGATCTCCGAGTCCGCGGACGATGATGATGATGATGATGAT 540  
Db 717 AAGGCTTGCTCAAGTGAAGTAAATGATCTCCGAGTCCGCGGACGATGATGATGATGATGATGAT 776  
Qy 541 GACAGTGTCTGTTGCGGAAACCAACGAAGCGTACCTCGGACCAACTACCGCAAGGCTGGC 600  
Db 777 GACAGTGTCTGTTGCGGAAACCAACGAAGCGTACCTCGGACCAACTACCGCAAGGCTGGC 836  
Qy 601 ATGGCTTACGTCATCGAGGATCTACTGCACTTCTGCGGCTGATGATGATGATGATGATGATGAT 660  
Db 837 ATGGCTTACGTCATCGAGGATCTACTGCACTTCTGCGGCTGATGATGATGATGATGATGATGAT 896  
Qy 661 GACAAATCCATTAAGGAGTAAATGATCTCCGATCGCGGCGAGATGATGATGATGATGATGATGAT 720  
Db 897 GACAAATCCATTAAGGAGTAAATGATCTCCGATCGCGGCGAGATGATGATGATGATGATGATGAT 956  
Qy 721 GAGCAGCGCAACTGTTGGAAGAAATCCAGCGGTACTACCTGAATACGCTCGGATCTAT 780  
Db 957 GAGCAGCGCAACTGTTGGAAGAAATCCAGCGGTACTACCTGAATACGCTCGGATCTAT 1016  
Qy 781 ATCTGAAACAGCTGAGCGGTCGCGGCTTCTGCGGCTGATGATGATGATGATGATGATGATGAT 840  
Db 1017 ATCTGAAACAGCTGAGCGGTCGCGGCTTCTGCGGCTGATGATGATGATGATGATGATGATGAT 1076  
Qy 841 ATCTCTCTGAGTACGACGCTCGGATGCAAAACTCCAACTGTCATCTCCCTCAAG 900  
Db 1077 ATCTCTCTGAGTACGACGCTCGGATGCAAAACTCCAACTGTCATCTCCCTCAAG 1136  
Qy 901 CTGAAGACAGAAAGCTGCGGCTTCTCGAGGAGATCTGGGATGTTGGC-GGACATGTC 959  
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Db 1137 CTCAAGAACAGAAAGCTGCGCCCTTTCTCGAGAGATCGGATGTGGCAGGACATGTC 1196  
Qy 960 GCACACCCACCGCGGCTATCTCGAGTCCCGCCACGAATCTTAGCCCTGCGGCACG 1019  
Db 1197 GCACACCCACCGCGGCTAT-CTCGAGTCCCGCCACGAATCTTAGCCCTGCGGCACG 1255  
Qy 1020 CATCGCGGATGCGCGGCTCGCGGCGCGCTGCTCTGA 1054  
Db 1256 CATCGCGGATGCGCGGCTCGCGGCGCGCTGCTCTGA 1290

## RESULT 10

US-09-965-697-14  
; Sequence 14, Application US/09965697  
; Patent No. US20020110861A1  
; GENERAL INFORMATION:  
; APPLICANT: Hormann, Robert E.  
; APPLICANT: Palli, Subba Reddy  
; APPLICANT: Carlson, Glenn R.  
; APPLICANT: Cress, Dean E.  
; APPLICANT: Dhadiella, Tarlochan S.  
; APPLICANT: Herzig, Ronald P.  
; APPLICANT: Rudla, Arthur J.  
; APPLICANT: Philip, Mohan  
; TITLE OF INVENTION: Multiple Inducible Gene Regulation System  
; FILE REFERENCE: RH-0036 (DN A01115A)  
; CURRENT APPLICATION NUMBER: US/09/965,697  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 1073  
; TYPE: DNA  
; ORGANISM: Choristoneura fumiferana  
US-09-965-697-14

Query Match 95.8%; Score 1010.2; DB 3; Length 1073;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 1047; Conservative 0; Mismatches 3; Indels 5; Gaps 3;

Qy 1 CCTGAGTGGCTAGTACCGGAGACTCAGTGGCCCATGAAGCGGAAAGAGAAAGACACAG 60  
Db 1 CCTGAGTGGCTAGTACCGGAGACTCAGTGGCCCATGAAGCGGAAAGAGAAAGACACAG 60  
Qy 61 AAGGAGAGGACAAATGCTCTGTGACGACGAGCGGTGGACGACACATGCGGCCCAT 120  
Db 61 AAGGAGAGGACAAATGCTCTGTGACGACGAGCGGTGGACGACACATGCGGCCCAT 120  
Qy 121 ATGCAAGTGAACCTCCACTCTCTGAAGGAGGAGGATTCAGAGTGGTCCGAGGTTT 180  
Db 121 ATGCAAGTGAACCTCCACTCTCTGAAGGAGGAGGATTCAGAGTGGTCCGAGGTTT 180  
Qy 181 CTCTCCGACAGCTGTTGGAGACAAACCGGACGAAACATCCCGAGTTGACAGCCAAC 240  
Db 181 CTCTCCGACAGCTGTTGGAGACAAACCGGACGAAACATCCCGAGTTGACAGCCAAC 240  
Qy 241 CAGCAGTTCCTTATGCGCAGGCTCATCTGGTACGAGCGGGTACGAGCGGCTTCTGAT 300  
Db 241 CAGCAGTTCCTTATGCGCAGGCTCATCTGGTACGAGCGGGTACGAGCGGCTTCTGAT 300  
Qy 301 GAAGATTTGAAGAGGATTCGACAGCTGCGAGCGGACGAGATGAAGAGAGTCT 360  
Db 301 GAAGATTTGAAGAGGATTCGACAGCTGCGAGCGGACGAGATGAAGAGAGTCT 360  
Qy 361 GACACTCCCTCCCGCAGATCAGAGATGACTATCTCAGGTCCAACTTATCGTGGAG 420  
Db 361 GACACTCCCTCCCGCAGATCAGAGATGACTATCTCAGGTCCAACTTATCGTGGAG 420  
Qy 421 TTCCGAGGAGGATTTGCCAGGTTCCGCAAGATTCGAGGCTGATCAAAATTAAGCTGCTT 480  
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Qy 481 AAGGCTTGCTCAAGTGAGGTAAATGATGCTCGAGTGGCGGAGCATACGATGGGCTCA 540  
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Qy 541 GACAGTGTCTGTTCCGGAACAAACCAAGCGTACACTCGCGCAACACTACCGCAAGGCTGGC 600  
Db 538 GACAGTGTCTGTTCCGGAACAAACCAAGCGTACACTCGCGCAACACTACCGCAAGGCTGGC 597  
Qy 601 ATGGCTTACGTTCATCGAGGATCTACTGCACTTTCTGCCGTTGCAATGATCTCTATGGGTTG 660  
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Db 658 GACACATCCATTCAGCGCTGCTCAGCGGTGCTGATCTTTTCTGACCGGCGAGGTTG 717  
Qy 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACTGATAGCTCCGATCTAT 780  
Db 718 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACTGATAGCTCCGATCTAT 777  
Qy 781 ATCTGAACCAAGTGAAGCGGTGCGCGCTTCGTTCGTATATACGGCAAGATCTCTCA 840  
Db 778 ATCTGAACCAAGTGAAGCGGTGCGCGCTTCGTTCGTATATACGGCAAGATCTCTCA 837  
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Qy 901 CTCAAGAACAGAAAGCTGCGGCTTTCTTCGAGGAGATCTGGGATGTGGC-GGACATGTC 959  
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Qy 960 GCACACCCACCGGCTTATCTCGAGTCCCGCCACGAATCTTAGCCCTTGGCGCACG 1019  
Db 958 GCACACCCACCGGCTTAT-CTCGAGTCCCGCCACGAATCTTAGCCCTTGGCGCACG 1016  
Qy 1020 CATCGCGGATGCGGCTCGCGGCGGCTGCTCTGA 1054  
Db 1017 CATCGCGGATGCGGCTCGCGGCGGCTGCTCTGA 1051

## RESULT 11

US-10-614-116-1  
; Sequence 1, Application US/10614116  
; Publication No. US20040049037A1  
; GENERAL INFORMATION:  
; APPLICANT: Tice, Colin M  
; APPLICANT: Hormann, Robert E  
; APPLICANT: Michelotti, Enrique L  
; TITLE OF INVENTION: Ketones for modulating the expression of exogenous genes via an  
; FILE REFERENCE: A01386us  
; CURRENT APPLICATION NUMBER: US/10/614,116  
; CURRENT FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/393,960  
; PRIOR FILING DATE: 2002-07-05  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1073  
; TYPE: DNA  
; ORGANISM: Choristoneura fumiferana  
US-10-614-116-1

Query Match 95.8%; Score 1010.2; DB 7; Length 1073;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 1047; Conservative 0; Mismatches 3; Indels 5; Gaps 3;

Qy 1 CCTGAGTGGCTAGTACCGGAGACTCAGTGGCCCATGAAGCGGAAAGAGAAAGACACAG 60  
Db 1 CCTGAGTGGCTAGTACCGGAGACTCAGTGGCCCATGAAGCGGAAAGAGAAAGACACAG 60

QY 61 AAGGAGGACCAAACTGCTGTGACGACGACGAGCGGTGACGACCAACATGCGCCCAATT 120  
Db 61 AAGGAGGACCAAACTGCTGTGACGACGACGAGCGGTGACGACCAACATGCGCCCAATT 120  
QY 121 ATGCAGTGTGAACCTCCACCTCTGAAGCAGCAGGATTCACGAAGTGGTCCCAAGGTTT 180  
Db 121 ATGCAGTGTGAACCTCCACCTCTGAAGCAGCAGGATTCACGAAGTGGTCCCAAGGTTT 180  
QY 181 CTCTCCGACAAGCTGTTGGAGACAAACCGGAGAGAAACATCCCCCAAGTTGACAGCCAAC 240  
Db 181 CTCTCCGACAAGCTGTTGGAGACAAACCGGAGAGAAACATCCCCCAAGTTGACAGCCAAC 240  
QY 241 CAGCAGTTCCTTATCGCAGGCTCATCTGTGACGACGAGCGGTGACGAGCGCTTCTGAT 300  
Db 241 CAGCAGTTCCTTATCGCAGGCTCATCTGTGACGACGAGCGGTGACGAGCGCTTCTGAT 300  
QY 301 GAAGATTTGAAGAGGATTAAGCAGAGCTGCGCAGCAAGCGGACGATGAAACGAAGAGTCT 360  
Db 301 GAAGATTTGAAGAGGATTAAGCAGAGCTGCGCAGCAAGCGGACGATGAAACGAAGAGTCT 360  
QY 361 GACACTCCCTTCCGCGCAGATCAAGAGATGACTATCTCAGGTCCTCAACTTATCGTGGAG 420  
Db 361 GACACTCCCTTCCGCGCAGATCAAGAGATGACTATCTCAGGTCCTCAACTTATCGTGGAG 420  
QY 421 TTCCGAGAGGATTCGACAGGTTCCGCAAGATCTCGAGCGCTGATCAAAATACGCTGCTT 480  
Db 421 TTCCGAGAGGATTCGACAGGTTCCGCAAGATCTCGAGCGCTGATCAAAATACGCTGCTT 480  
QY 481 AAGGCTTGCTCAAGTGAAGTAAATGATGCTCCGAGTGGCGAGCATACGATGCGGCTCA 540  
Db 481 AAGGCTTGCTCAAGTGAAGTAAATGATGCTCCGAGTGGCGAGCATACGATGCGGCTCA 540  
QY 541 GACAGTGTCTTCTGTTCCGCAACCAAGCGGTACACTCGCGACCAACTACCGCAAGGCTGGC 600  
Db 541 GACAGTGTCTTCTGTTCCGCAACCAAGCGGTACACTCGCGACCAACTACCGCAAGGCTGGC 600  
QY 598 ATGGCTTACGCTCATCGAGGATCTACTGCACTTCTGCGGTCGATGACTCTATGGCGTTG 657  
Db 598 ATGGCTTACGCTCATCGAGGATCTACTGCACTTCTGCGGTCGATGACTCTATGGCGTTG 657  
QY 661 GACAAATCCATTAAGCGCTGCTCAGCGCTGCTCATCTTTTCTGACCGCGGCTTG 720  
Db 661 GACAAATCCATTAAGCGCTGCTCAGCGCTGCTCATCTTTTCTGACCGCGGCTTG 720  
QY 717 GACAAATCCATTAAGCGCTGCTCAGCGCTGCTCATCTTTTCTGACCGCGGCTTG 717  
Db 717 GACAAATCCATTAAGCGCTGCTCAGCGCTGCTCATCTTTTCTGACCGCGGCTTG 717  
QY 721 GAGCAGCGCAACTGCTGGAAGAAATCCAGCGGTACTACCTGAATACGCTCCGCACTAT 780  
Db 721 GAGCAGCGCAACTGCTGGAAGAAATCCAGCGGTACTACCTGAATACGCTCCGCACTAT 780  
QY 778 ATCTGAAACCAAGCTGAGCGGTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837  
Db 778 ATCTGAAACCAAGCTGAGCGGTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 837  
QY 841 ATCTGCTGAGCTGAGCGGTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db 841 ATCTGCTGAGCTGAGCGGTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
QY 898 CTCAAGAACAGAAAGCTGCGGCTTCTCTCGAGGAGATCTGGGATGTCGAGGATGTC 957  
Db 898 CTCAAGAACAGAAAGCTGCGGCTTCTCTCGAGGAGATCTGGGATGTCGAGGATGTC 957  
QY 960 GCACACCCAAACCGCGCTTATCTCGAGTCCCAAGATCTTAGCCCTGCGCGCAG 1019  
Db 960 GCACACCCAAACCGCGCTTATCTCGAGTCCCAAGATCTTAGCCCTGCGCGCAG 1019  
QY 1020 CATCGCGGATGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054  
Db 1020 CATCGCGGATGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054  
QY 1017 CATCGCGGATGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051  
Db 1017 CATCGCGGATGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051

RESULT 12

US-10-460-820-1

; Sequence 1, Application US/10460820

; Publication No. US20050228016A1

GENERAL INFORMATION:  
; APPLICANT: Michelotti, Enrique L  
; APPLICANT: Tice, Colin M  
; APPLICANT: Palli, Subba R  
; APPLICANT: Thompson, Christine S  
; APPLICANT: Dhadialla, Tarlochan S  
; TITLE OF INVENTION: Tetrahydroquinolines for Modulating the Expression of Exogenous  
; FILE REFERENCE: A01378-US  
; CURRENT FILING DATE: 2003-06-12  
; PRIOR APPLICATION NUMBER: US 60/388,353  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1073  
; TYPE: DNA  
; ORGANISM: Choristoneura fumiferana  
US-10-460-820-1

Query Match 95.8%; Score 1010.2; DB 9; Length 1073;

Best Local Similarity 99.2%; Pred. No. 0;

Matches 1047; Conservative 0; Mismatches 3; Indels 5; Gaps 3;

QY 1 CTGAGTGTGATGATACCGAGACTCAGTGGCCCATGAGCGGAAAGAGAAAGCAG 60  
Db 1 CTGAGTGTGATGATACCGAGACTCAGTGGCCCATGAGCGGAAAGAGAAAGCAG 60  
QY 61 AAGGAGAGGACAACTGCTGTGACGACGACGAGCGGTGACGACCAACATGCGCCCAATT 120  
Db 61 AAGGAGAGGACAACTGCTGTGACGACGACGAGCGGTGACGACCAACATGCGCCCAATT 120  
QY 121 ATGCAGTGTGAACCTCCACCTCTGAAGCAGCAGGATTCACGAAGTGGTCCCAAGGTTT 180  
Db 121 ATGCAGTGTGAACCTCCACCTCTGAAGCAGCAGGATTCACGAAGTGGTCCCAAGGTTT 180  
QY 181 CTCTCCGACAAGCTGTTGGAGACAAACCGGAGAGAAACATCCCCCAAGTTGACAGCCAAC 240  
Db 181 CTCTCCGACAAGCTGTTGGAGACAAACCGGAGAGAAACATCCCCCAAGTTGACAGCCAAC 240  
QY 241 CAGCAGTTCCTTATCGCAGGCTCATCTGTGACGACGAGCGGTGACGAGCGCTTCTGAT 300  
Db 241 CAGCAGTTCCTTATCGCAGGCTCATCTGTGACGACGAGCGGTGACGAGCGCTTCTGAT 300  
QY 301 GAAGATTTGAAGAGGATTAAGCAGAGCTGCGCAGCAAGCGGACGATGAAACGAAGAGTCT 360  
Db 301 GAAGATTTGAAGAGGATTAAGCAGAGCTGCGCAGCAAGCGGACGATGAAACGAAGAGTCT 360  
QY 361 GACACTCCCTTCCGCGCAGATCAAGAGATGACTATCTCAGGTCCTCAACTTATCGTGGAG 420  
Db 361 GACACTCCCTTCCGCGCAGATCAAGAGATGACTATCTCAGGTCCTCAACTTATCGTGGAG 420  
QY 421 TTCCGAGAGGATTCGACAGGTTCCGCAAGATCTCGAGCGCTGATCAAAATACGCTGCTT 480  
Db 421 TTCCGAGAGGATTCGACAGGTTCCGCAAGATCTCGAGCGCTGATCAAAATACGCTGCTT 480  
QY 481 AAGGCTTGCTCAAGTGAAGTAAATGATGCTCCGAGTGGCGAGCATACGATGCGGCTCA 540  
Db 481 AAGGCTTGCTCAAGTGAAGTAAATGATGCTCCGAGTGGCGAGCATACGATGCGGCTCA 540  
QY 541 GACAGTGTCTTCTGTTCCGCAACCAAGCGGTACACTCGCGACCAACTACCGCAAGGCTGGC 600  
Db 541 GACAGTGTCTTCTGTTCCGCAACCAAGCGGTACACTCGCGACCAACTACCGCAAGGCTGGC 600  
QY 598 ATGGCTTACGCTCATCGAGGATCTACTGCACTTCTGCGGTCGATGACTCTATGGCGTTG 657  
Db 598 ATGGCTTACGCTCATCGAGGATCTACTGCACTTCTGCGGTCGATGACTCTATGGCGTTG 657  
QY 661 GACAAATCCATTAAGCGCTGCTCAGCGCTGCTCATCTTTTCTGACCGCGGCTTG 720  
Db 661 GACAAATCCATTAAGCGCTGCTCAGCGCTGCTCATCTTTTCTGACCGCGGCTTG 720  
QY 717 GACAAATCCATTAAGCGCTGCTCAGCGCTGCTCATCTTTTCTGACCGCGGCTTG 717  
Db 717 GACAAATCCATTAAGCGCTGCTCAGCGCTGCTCATCTTTTCTGACCGCGGCTTG 717

QY 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACTGAATACGCTCCGATCTAT 780  
DB 718 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACTGAATACGCTCCGATCTAT 777  
QY 781 ATCTGAAACAGCTGAGCGGTCGGCGGTTGCTCGGTATATACGCGCAAGATCTCTCTCA 840  
DB 778 ATCTGAAACAGCTGAGCGGTCGGCGGTTGCTCGGTATATACGCGCAAGATCTCTCTCA 837  
QY 841 ATCTCTCTGAGTACGACGCTCGGCGATGCAAAATCTCCAGATGCTCTCTCTCAAG 900  
DB 838 ATCTCTCTGAGTACGACGCTCGGCGATGCAAAATCTCCAGATGCTCTCTCTCAAG 897  
QY 901 CTCAAGAACAGAAAGCTGCGCGCTTTCTCTGAGAGATCTGGGATGTCGCG-GGACATGTC 959  
DB 898 CTCAAGAACAGAAAGCTGCGCGCTTTCTCTGAGAGATCTGGGATGTCGAGAGATGTC 957  
QY 960 GCACACCCAAACCGCGCTATCTCTGAGTCCCGCAAGATCTCTAGCCCTCGCGCACG 1019  
DB 958 GCACACCCAAACCGCGCTAT-CTCGAGTCCCGCAAGATCTCTAGCCCTCGCGCACG 1016  
QY 1020 CATCGCGGATCGCGGTCGGCGCGGCTGCTCTGA 1054  
DB 1017 CATCGCGGATCGCGGTCGGCGCGGCTGCTCTGA 1051

## RESULT 13

US-09-965-703-2  
; Sequence 2, Application US/09965703  
; Patent No. US20020119521A1  
; GENERAL INFORMATION:  
; APPLICANT: Rohm and Haas Company  
; APPLICANT: Palli, Subba Reddy  
; APPLICANT: Kapitskaya, Marianna Zinovjevna  
; APPLICANT: Cress, Dean Ervin  
; TITLE OF INVENTION: No. US20020119521A1el Bcdysone Receptor-Based Inducible Gene Expr  
; FILE REFERENCE: A01020B  
; CURRENT APPLICATION NUMBER: US/09/965,703  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/191,355  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 60/269,799  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: PCT/US01/09050  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 1110  
; TYPE: DNA  
; ORGANISM: Choristoneura fumiferana  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: No. US20020119521A1el Sequence  
US-09-965-703-2

Query Match 95.4%; Score 1005; DB 3; Length 1110;  
Best Local Similarity 100.0%; Pred. No. 8.1e-314;  
Matches 1005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACAG 60  
DB 106 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACAG 165  
QY 61 AAGAGAAAGACAACTGCTGTGACGACGCGGTGGACGACCAATGCGCGCCATT 120  
DB 166 AAGAGAAAGACAACTGCTGTGACGACGCGGTGGACGACCAATGCGCGCCATT 225  
QY 121 ATGCAAGTGAACCTCACTCTGAGAGCAAGGATTCAGAGTGGTCCCAAGTTT 180  
DB 226 ATGCAAGTGAACCTCACTCTGAGAGCAAGGATTCAGAGTGGTCCCAAGTTT 285  
QY 181 CTCTCCCAAGAGCTGTTGGAGACAAACCGGCGAGAAAACATCCCGCAAGTTTGACAGCCAAC 240

DB 286 CTCTCCGACAAAGCTGTGTGGAGACAAACCGCGAGAAAACATCCCGAGTTGACAGCCAAC 345  
QY 241 CAGCAGTTCTTATCGCAGAGGCTCATCTGTGTACAGGACGGGTACGAGAGGCTTCTCAT 300  
DB 346 CAGCAGTTCTTATCGCAGAGGCTCATCTGTGTACAGGACGGGTACGAGAGGCTTCTCAT 405  
QY 301 GAAGATTTGAAGAGATTTACGACAGCTGGCAGCAGCGGACGAGCGATGAAACGAGGTCT 360  
DB 406 GAAGATTTGAAGAGATTTACGACAGCTGGCAGCAGCGGACGAGCGATGAAACGAGGTCT 465  
QY 361 GACACTCCCTTCGCGCAGATCAACAGAGATGACTATCTCACGCTCCAACTTATCTGGAG 420  
DB 466 GACACTCCCTTCGCGCAGATCAACAGAGATGACTATCTCACGCTCCAACTTATCTGGAG 525  
QY 421 TTGCGGAAGGATTTGCGCAGGTTTCCCAAGATCTCTCGAGCTTGATCAAAATTAAGCTGTT 480  
DB 526 TTGCGGAAGGATTTGCGCAGGTTTCCCAAGATCTCTCGAGCTTGATCAAAATTAAGCTGTT 585  
QY 481 AAGGCTTGTCTCAAGTGAGTAAATGATCTCCGAGTCCGCGCAGATACGATCGGCCTCA 540  
DB 586 AAGGCTTGTCTCAAGTGAGTAAATGATCTCCGAGTCCGCGCAGATACGATCGGCCTCA 645  
QY 541 GACAGTGTCTCTTCGCGAAACCAACAGCGTACACTTCGCGACAACTACCGCAAGGCTGCG 600  
DB 646 GACAGTGTCTCTTCGCGAAACCAACAGCGTACACTTCGCGACAACTACCGCAAGGCTGCG 705  
QY 601 ATGGCTTACGTCATCGAGGATCTACTGCACTTTTCGCGGTGATGTACTTATGCGGTG 660  
DB 706 ATGGCTTACGTCATCGAGGATCTACTGCACTTTTCGCGGTGATGTACTTATGCGGTG 765  
QY 661 GACAACTCATTTAGCGCTGCTCAAGCTGCTCAAGCTGCTCAAGCTGCTCAAGCTGCTCA 720  
DB 766 GACAACTCATTTAGCGCTGCTCAAGCTGCTCAAGCTGCTCAAGCTGCTCAAGCTGCTCA 825  
QY 721 GAGCAGCCCAACTGTGTGAAGAAATCCAGCGGTACTACTGAATACGCTCCGATCTAT 780  
DB 826 GAGCAGCCCAACTGTGTGAAGAAATCCAGCGGTACTACTGAATACGCTCCGATCTAT 885  
QY 781 ATCTGAAACAGCTGAGCGGTCGGCGGTTGCTCGGTATATAGCGCAAGATCTCTCTCA 840  
DB 886 ATCTGAAACAGCTGAGCGGTCGGCGGTTGCTCGGTATATAGCGCAAGATCTCTCTCA 945  
QY 841 ATCTCTCTGAGTACGACGCTCGGCAATGCAAAATCCAAATGTCATCTCCCTCAAG 900  
DB 946 ATCTCTCTGAGTACGACGCTCGGCAATGCAAAATCCAAATGTCATCTCCCTCAAG 1005  
QY 901 CTCAAGAACAGAAAGCTGCGCGCTTTCTCTCGAGGAGATCTGGGATGTGGCGACATGTCG 960  
DB 1006 CTCAAGAACAGAAAGCTGCGCGCTTTCTCTCGAGGAGATCTGGGATGTGGCGACATGTCG 1065  
QY 961 CACACCCAAACCGCGCTTATCTCTGAGTCCCGCAAGATCTCTAG 1005  
DB 1066 CACACCCAAACCGCGCTTATCTCTGAGTCCCGCAAGATCTCTAG 1110

## RESULT 14

US-10-239-134-2  
; Sequence 2, Application US/10239134  
; Publication No. US20040033600A1  
; GENERAL INFORMATION:  
; APPLICANT: Rohm and Haas Company  
; APPLICANT: Palli, Subba Reddy  
; APPLICANT: Kapitskaya, Marianna Zinovjevna  
; APPLICANT: Cress, Dean Ervin  
; TITLE OF INVENTION: No. US20040033600A1el Bcdysone Receptor-Based Inducible Gene Expr  
; FILE REFERENCE: RH0020  
; CURRENT APPLICATION NUMBER: US/10/239,134  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: 60/191,355  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 60/269,799  
; PRIOR FILING DATE: 2001-02-20  
; NUMBER OF SEQ ID NOS: 64

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20040033600A1el Sequence
US-10-239-134-2

Query Match          95.4%; Score 1005; DB 7; Length 1110;
Best Local Similarity 100.0%; Pred. No. 8.1e-314;
Matches 1005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAGTGGCTAGTACCGAGACTCAGTGCCTCCATGAAGCGCCCATGAAGCGAAAGAGAAAGCAAG 60
Db 106 CCTGAGTGGCTAGTACCGAGACTCAGTGCCTCCATGAAGCGCCCATGAAGCGAAAGAGAAAGCAAG 165
Qy 61 AAGGAGAGGACAAACTGCCTGTGAGCAAGCGAGCGGTGGAGCGACCATGCGCGCCCATTT 120
Db 166 AAGGAGAGGACAAACTGCCTGTGAGCAAGCGAGCGGTGGAGCGACCATGCGCGCCCATTT 225
Qy 121 ATGCAGTGTGAACCTCCACCTCTCTGAAGCAAGGATTCACGAAGTGGTCCCAAGGTTT 180
Db 226 ATGCAGTGTGAACCTCCACCTCTCTGAAGCAAGGATTCACGAAGTGGTCCCAAGGTTT 285
Qy 181 CTCTCCGACAGCTGTGTGGAGACAAACCGGCGAGAAAACATCCCCAGTTTGACAGCCAAAC 240
Db 286 CTCTCCGACAGCTGTGTGGAGACAAACCGGCGAGAAAACATCCCCAGTTTGACAGCCAAAC 345
Qy 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGACAGACGGGTACGAGCGCTTCTGTAT 300
Db 346 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGACAGACGGGTACGAGCGCTTCTGTAT 405
Qy 301 GAGCATTTGAAGAGGATTAACGACAGCTGGCGAGCAAGCGACGATGAAGAGAGTCT 360
Db 406 GAGCATTTGAAGAGGATTAACGACAGCTGGCGAGCAAGCGACGATGAAGAGAGTCT 465
Qy 361 GACATCCCTTCCGCCAGATCACAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420
Db 466 GACATCCCTTCCGCCAGATCACAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 525
Qy 421 TTCCGGAAGGATTCGCAAGGTTCCGCAAGATTCGCGAGCTGTATCAAAATACGCTGCTT 480
Db 526 TTCCGGAAGGATTCGCAAGGTTCCGCAAGATTCGCGAGCTGTATCAAAATACGCTGCTT 585
Qy 481 AAGGCTTGCTCAAGTGAAGTAATGATCTCGAGTCCGCGAGCAGATACGATGCGGCTCA 540
Db 586 AAGGCTTGCTCAAGTGAAGTAATGATCTCGAGTCCGCGAGCAGATACGATGCGGCTCA 645
Qy 541 GACAGTGTCTGTTCGCGAAACAAACGAGCTACACTCGCGACAACTACCGCAAGGCTGGC 600
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Qy 601 ATGCGCTTCACTGAGGATCTACTGACCTTTCGCGGTGTCATGTACTCTATGCGGTG 660
Db 706 ATGCGCTTCACTGAGGATCTACTGACCTTTCGCGGTGTCATGTACTCTATGCGGTG 765
Qy 661 GACAACTCCATTAAGCGCTGCTCAGCGCTGTCTGATCTTTCTGACCGCGCAGGTTG 720
Db 766 GACAACTCCATTAAGCGCTGCTCAGCGCTGTCTGATCTTTCTGACCGCGCAGGTTG 825
Qy 721 GAGCAGCGGCAACTGGTGGAGAAATCCAGCGGTACTACCTGAAATACGCTCCGATCTAT 780
Db 826 GAGCAGCGGCAACTGGTGGAGAAATCCAGCGGTACTACCTGAAATACGCTCCGATCTAT 885
Qy 781 ATCTGAAACCAAGCTGAGCGGTTCGCGGTTTCGTCCTCATATACGCGCAAGATCTCTCA 840
Db 886 ATCTGAAACCAAGCTGAGCGGTTCGCGGTTTCGTCCTCATATACGCGCAAGATCTCTCA 945
Qy 841 ATCTCTCTGAGCTACGCAAGCTTCGGCATGCAAAATCTCCAAACATGTGATCTCCCTCAAG 900
Db 946 ATCTCTCTGAGCTACGCAAGCTTCGGCATGCAAAATCTCCAAACATGTGATCTCCCTCAAG 1005
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Qy 901 CTCAGAAACAGAAAGCTGCGCCTTTCTCTCGAGAGATCTGGGATGTGGCGGACATGTG 960
Db 1006 CTCAGAAACAGAAAGCTGCGCCTTTCTCTCGAGAGATCTGGGATGTGGCGGACATGTG 1065
Qy 961 CACACCAACCGCGCTATCTCTCGAGTCCGCCACGATCTCTAG 1005
Db 1066 CACACCAACCGCGCTATCTCTCGAGTCCGCCACGATCTCTAG 1110

RESULT 15
US-09-965-703-58
; Sequence 58, Application US/09965703
; Patent No. US20020119521A1
; GENERAL INFORMATION:
; APPLICANT: Rohm and Haas Company
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kapitekaya, Marianna Zinovjevna
; APPLICANT: Cress, Dean Ervin
; TITLE OF INVENTION: No. US20020119521A1el Bcdysone Receptor-Based Inducible Gene Expr
; FILE REFERENCE: A01020B
; CURRENT APPLICATION NUMBER: US/09/965,703
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/09050
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Choristoneura fumiferana
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20020119521A1el Sequence
US-09-965-703-58

Query Match          95.4%; Score 1005; DB 3; Length 1542;
Best Local Similarity 100.0%; Pred. No. 8.1e-314;
Matches 1005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAGTGGCTAGTACCGAGACTCAGTGCCTCCATGAAGCGCCCATGAAGCGAAAGAGAAAGCAAG 60
Db 538 CCTGAGTGGCTAGTACCGAGACTCAGTGCCTCCATGAAGCGCCCATGAAGCGAAAGAGAAAGCAAG 597
Qy 61 AAGGAGAGGACAAACTGCCTGTGACGACGACGCGGTGGAGCGACCATGCGCGCCCATTT 120
Db 598 AAGGAGAGGACAAACTGCCTGTGACGACGACGCGGTGGAGCGACCATGCGCGCCCATTT 657
Qy 121 ATGCAGTGTGAACCTCCACCTCTCTGAGCAGCAGGATTCACGAGTGGTCCCAAGGTTT 180
Db 658 ATGCAGTGTGAACCTCCACCTCTCTGAGCAGCAGGATTCACGAGTGGTCCCAAGGTTT 717
Qy 181 CTCTCCGACAGCTGTGTGGAGACAAACCGGCGAGAAAACATCCCCAGTTTGACAGCCAAAC 240
Db 718 CTCTCCGACAGCTGTGTGGAGACAAACCGGCGAGAAAACATCCCCAGTTTGACAGCCAAAC 777
Qy 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGATCAGAGCGGTTACGAGCAGCCTTCTGTAT 300
Db 778 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGATCAGAGCGGTTACGAGCAGCCTTCTGTAT 837
Qy 301 GAGAGATTTGAAGAGATTAACGAGAGCTGGCAGCAAGCGGACGATGAAGAGAGTCT 360
Db 838 GAGAGATTTGAAGAGATTAACGAGAGCTGGCAGCAAGCGGACGATGAAGAGAGTCT 897
Qy 361 GACATCCCTTCCCGCAGATTCACAGAGATGACTATCTCAGCGTCCAACTTATCTGAGGAG 420
Db 898 GACATCCCTTCCCGCAGATTCACAGAGATGACTATCTCAGCGTCCAACTTATCTGAGGAG 957
Qy 421 TTCCGGAAGGATTCGCGGTTTCGCGGTTTCGCGGTTTCGCGGTTTCGCGGTTTCGCGGTTTCGCGGTT 480
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958	Db	TTCCGGAAGGATTTCCAGGGTTCCCAAGATCTCGCAGCGCTATCAAATTAACGCTGCTT	1017
481	QY	AAGGCTTCTCAAGCTGAGGTAATCATGCTCCGAGTCGGCGGAGCATACGATCGGGCTCA	540
1018	Db	AAGGCTTGCTCAAGTGAGGTAATGATGCTCCGAGTCGGCGGAGCATACGATCGGGCTCA	1077
541	QY	GACAGTGTCTGTTCGCGAAACAAACAAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC	600
1078	Db	GACAGTGTCTGTTCGCGAAACAAACAAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC	1137
601	QY	ATGGCCTACGTCATCGAGGATCTACTGCACTTCTGCGGTCGATGTACTCTATGGCGTTG	660
1138	Db	ATGGCCTACGTCATCGAGGATCTACTGCACTTCTGCGGTCGATGTACTCTATGGCGTTG	1197
661	QY	GACAACTATCCATTAAGCGCTGCTCAACGCGTGTCTGCATCTTTCTGACCGGCCAGGGTTG	720
1198	Db	GACAACTATCCATTAAGCGCTGCTCAACGCGTGTCTGCATCTTTCTGACCGGCCAGGGTTG	1257
721	QY	GAGCAGCGGCAACTGGTGGAAGAAATCCAGCGGTACTACCTGAATACGCTCCGGATCTAT	780
1258	Db	GAGCAGCGGCAACTGGTGGAAGAAATCCAGCGGTACTACCTGAATACGCTCCGGATCTAT	1317
781	QY	ATCCTGAACCAAGCTGAGCGGGTCGGCGGTTCGTCCTCATATATACGGCAAGATCCTCTCA	840
1318	Db	ATCCTGAACCAAGCTGAGCGGGTCGGCGGTTCGTCCTCATATATACGGCAAGATCCTCTCA	1377
841	QY	ATCCTCTCTGAGCTACGCAACGCTCGGCAATGCAAACTCCAAATATGTCATCTCCCTCAAG	900
1378	Db	ATCCTCTCTGAGCTACGCAACGCTCGGCAATGCAAACTCCAAATATGTCATCTCCCTCAAG	1437
901	QY	CTCAAGAAACAGAAAGCTGCGCCCTTTCTCTGAGGAGATCTGGGATGTGGCGGACATGTCG	960
1438	Db	CTCAAGAAACAGAAAGCTGCGCCCTTTCTCTGAGGAGATCTGGGATGTGGCGGACATGTCG	1497
961	QY	CACACCCGAACCGCGCCTATCCTCGAGTCCGCCCAAGAAATCTCTAG	1005
1498	Db	CACACCCGAACCGCGCCTATCCTCGAGTCCGCCCAAGAAATCTCTAG	1542

Search completed: January 31, 2006, 16:50:51  
Job time : 898 secs

Result No.	Score	Query Match		Length	DB	ID	Description
		Score	Match				
1	636.4	60.4	2126	3	US-09-393-839-1	Sequence 1, Appli	
2	623.4	59.1	2840	3	US-10-087-167-1	Sequence 1, Appli	
3	621.6	59.0	1500	3	US-10-087-167-67	Sequence 67, Appl	
4	621.6	59.0	1767	3	US-10-087-167-120	Sequence 120, App	
5	617.4	58.6	1863	3	US-10-087-167-136	Sequence 136, App	
6	617.2	58.6	1848	3	US-10-087-167-134	Sequence 134, App	
7	617	58.5	1518	3	US-10-087-167-93	Sequence 93, Appl	
8	617	58.5	3972	3	US-10-087-167-104	Sequence 104, App	
9	616.4	58.5	1428	3	US-10-087-167-128	Sequence 128, App	
10	616.4	58.5	1809	3	US-10-087-167-142	Sequence 142, App	
11	614.2	58.3	1515	3	US-10-087-167-75	Sequence 75, Appl	
12	614.2	58.3	1782	3	US-10-087-167-124	Sequence 124, App	
13	611.4	58.0	1509	3	US-10-087-167-65	Sequence 65, Appl	
14	611.4	58.0	1776	3	US-10-087-167-118	Sequence 118, App	
15	609.6	57.8	1533	3	US-10-087-167-79	Sequence 79, Appl	
16	609.6	57.8	1800	3	US-10-087-167-126	Sequence 126, App	
17	605.6	57.5	1500	3	US-10-087-167-69	Sequence 69, Appl	
18	605.6	57.5	1767	3	US-10-087-167-122	Sequence 122, App	
19	604	57.3	1524	3	US-10-087-167-77	Sequence 77, Appl	
20	603.2	57.2	1800	3	US-10-087-167-147	Sequence 147, App	
21	595.8	55.6	1934	3	US-08-653-648A-2	Sequence 2, Appli	
22	595.8	55.6	1934	3	US-09-564-418-2	Sequence 2, Appli	
23	595.8	55.6	1934	3	US-09-564-418-61	Sequence 61, Appl	
24	595.8	55.6	2464	3	US-08-653-648A-3	Sequence 3, Appli	





Db 1660 GACATGTGCTAGCGCTGCTCACCGCCATCGTTATATTTCTCAGACCGGCCAGGCGTC 1719  
Qy 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACCTGAATACGCTCCGCACTTAT 780  
Db 1720 GAGCAACCCCTTTAGTGGAGAAATCCAGAGATACTACTTTGAAGAGCGCTCGGGTTTAC 1779  
Qy 781 ATCTGACACAGCTGAGCGGGTCGGCGGTTGCTCGCTCATATATACGGCAAGATCTCTCA 840  
Db 1780 ATTTTAAATCAGCAGCGCGCTCGCTCGCTCGCGCGGTGCTTTCGGCAAGATCTCGGC 1839  
Qy 841 ATCTCTCTGAGCTACGCAAGCTCGGATGCAAACTCCAACTGTCATCTCCCTCAAG 900  
Db 1840 GTGCTGAGGAACTGCGGCAAGCTGCGCAGCAAACTCCAACTGTCATCTCGCTGAAG 1899  
Qy 901 CTCAAGAACAGAAAGCTGCGCCCTTTCTCGAGGAGATCTGGGATGTGGCGGACATGTG 960  
Db 1900 CTGAAGAACAGAAACTTCCGCCATTTCTCGAGGAGATCTGGGAGCTGGCGGAGTGTG 1959  
Qy 961 CACACCCACCGCGCC 977  
Db 1960 ACGACGCGCGCGGCC 1976

## RESULT 3

US-10-087-167-67.  
; Sequence 67, Application US/10087167  
; Patent No. 6958236  
; GENERAL INFORMATION:  
; APPLICANT: Pascal, Erica  
; APPLICANT: Valentine, Scott  
; APPLICANT: Brown, Jeffrey  
; APPLICANT: Cockrell, Adam  
; APPLICANT: Johnson, Brian  
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS  
; FILE REFERENCE: 50018A  
; CURRENT APPLICATION NUMBER: US/10/087,167  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 1500  
; TYPE: DNA  
; ORGANISM: Synthetic construct  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1500)  
; OTHER INFORMATION: Ecdysone Receptor chimera MEV  
US-10-087-167-67

Query Match 59.0%; Score 621.6; DB 3; Length 1500;  
Best Local Similarity 78.5%; Pred. No. 9.8e-169;  
Matches 744; Conservative 0; Mismatches 204; Indels 0; Gaps 0;  
Qy 1 CCTGAGTGGCTAGTACCGGAGCTCAGTGGCCCATGAAGCGGAAAGAGAAAGACAG 60  
Db 310 CCGAGTGGCTGGTCCAGAGTCCAGTGGCAAGAACAAAGAGAAAGAGAGACAG 369  
Qy 61 AAGGAGAGGACAACTGCTGTCAGCAAGCGAGCGGTGAGACCAATGCGCCCAT 120  
Db 370 AGAGAAAAGACAACTGCCAGTCCAGTACGACGACAGTGGACGATCATATGCTGCCATA 429  
Qy 121 ATGCAAGTGAACCTCCCTGAGACGACGAGGATTCAGGAGTGGTCCCAAGTTT 180  
Db 430 ATGCAAGTGAACCTCCCTGAGACGACGAGGATTCAGGAGTGGTCCCAAGTTT 489  
Qy 181 CTCTCCGACAGCTGTTGGAGACAAACCGGACGAAACATCCCGAGTTGACAGCCAAC 240  
Db 490 CTAACGGAGAGCTAATGGAGCAGACAGACTGAAGATGTGACGCGCTGTGGCGGAC 549  
Qy 241 CAGCAGTTCCTTATCGCAGGCTCATCTGGTACAGGACGGGTACGAGCAGCTTCTGAT 300  
Db 241 CAGCAGTTCCTTATCGCAGGCTCATCTGGTACAGGACGGGTACGAGCAGCTTCTGAT 300

Db 550 CAGAAGTCCCTGATTCGCGAGGCTGTTGTGTGTAACAGGACGGATACGAGCAGCCTTCGGAA 609  
Qy 301 GAAGATTTGAAGAGGATTACGCGAGACGTCGAGCAGCAAGCGACGATGAAAAACGAGAGTCT 360  
Db 610 GAGGATCTCAAAGGGGTGACGCGAGCTTGGCAATCAGCAGATGAAGAGAGCAGAGACTCA 669  
Qy 361 GACACTCCCTTCGCGCAGATCAAGAGATGACTATCTCAAGGTCCTCACTTATGCTGGAG 420  
Db 670 GACATGTCATTCGCGCAGATCAAGAAATGACCATCTCAGAGTACAGCTAATAGTGGAG 729  
Qy 421 TTGCGGAAGGATTTGCGCAGGTTGCGCAAGATCTCGCAGCTGATCAAAATAGCTGCTT 480  
Db 730 TTTGCGCAAGGCTTACCTGGTCTTTCAAGATCTCAACCTGACCATGATCAATATTA 789  
Qy 481 AAGGCTTTGCTCAAGTGAAGTAAATGATCTCGGAGTCCGCGAGCAATACGATGCGGCCCTCA 540  
Db 790 AAGGCTGCTCAAGCGAAGTGAATGATCTCGGAGTAGAGGCGGTACGAGCGGTGTCG 849  
Qy 541 GACAGTGTCTGTTGCGCAACAAAGCGTACACTCGCGCAAACTACCGCAAGGCTGGC 600  
Db 850 GATAGCGTCTGTTGCGCAACAAAGCGGTACACTCGCGCAAACTACCGCAAGGCGGC 909  
Qy 601 ATGCGCTACGTCATCGAGGATCTACTGCACTTCTGCGGTCGATCTTATGCGGCTTG 660  
Db 910 ATGCGCTACGTCATCGAAGACCTGCTGCACTTCTGCGGTCGATCTTATGCGGCTTG 969  
Qy 661 GACAACTCCATTTACGCGCTGCTCAGCGTGTGCTCATCTTTTCTGACCGCGCAGGCTTG 720  
Db 970 GACAACTGATTTACGCGCTCTCTCATGCGCATGTTATATCTCGGATCGCGCGGCTA 1029  
Qy 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGTACTACTGTAATAGCTTCGCGCATCTAT 780  
Db 1030 GAGCAGCGCAACTGGTGGAGAAATCCAGCGTACTACTGTAATAGCTTCGCGCATCTAT 1089  
Qy 781 ATCTGACACGCTGAGCGGTCGCGCGCTGCTGCGTGCATATATACGCAAGATCTCTCA 840  
Db 1090 ATCATGAACCAAGCAGCAGCGCTGCGCGCTGCTGCGCGCTCATCTACGCAAGATTTCTG 1149  
Qy 841 ATCTCTCTGAGCTAGCAGCGCTGCGCGCTGCGCGCTGCGCGCTCATCTACGCAAGATTTCTG 900  
Db 1150 GTGCTTACCGGTTGCGGAGCTGGGCGATGCGAGATTCGCAATGTCATCTGCTGAG 1209  
Qy 901 CTCAAGAACAGAAAGTGGCGCTTTCTCGAGGAGATCTGGGATGTG 948  
Db 1210 CTCAAGAACAGAAAGTGGCGCTTTCTCGAGGAGATCTGGGAGCTG 1257

## RESULT 4

US-10-087-167-120  
; Sequence 120, Application US/10087167  
; Patent No. 6958236  
; GENERAL INFORMATION:  
; APPLICANT: Pascal, Erica  
; APPLICANT: Valentine, Scott  
; APPLICANT: Brown, Jeffrey  
; APPLICANT: Cockrell, Adam  
; APPLICANT: Johnson, Brian  
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS  
; FILE REFERENCE: 50018A  
; CURRENT APPLICATION NUMBER: US/10/087,167  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 120  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Synthetic Construct  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1767)  
; OTHER INFORMATION: Ecdysone receptor chimera G(M)EV

US-10-087-167-120

```

Query Match      59.0%; Score 621.6; DB 3; Length 1767;
Best Local Similarity 78.5%; Pred. No. 16-168;
Matches 744; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

QY 1 CCTGAGTGGCTAGTACCGGAGCTCAGTGGCCATGAAGCGGAAGAAAGAAAGCAG 60
DB 577 CCGAGTGGCTGTCCAGAGTCACTGTCAGAACAAAGAAAGAAAGAAAGCAG 636

QY 61 AAGGAGAGGACAACTGCTGTGACGACGAGCGGTGACGACCAATGCGGCCATT 120
DB 637 AGAGAAAGACAACTGCGAGTCACTGACGACGAGCGGTGACGACCAATGCGGCCATT 696

QY 121 ATGCAATGTGAACCTGCTGAGAGGAGGAGGATTCAGCAAGTGGTCCCAAGTTT 180
DB 697 ATGCAATGTGAACCTGCTGAGAGGAGGAGGATTCAGCAAGTGGTCCCAAGTTT 756

QY 181 CTCTCCGACAAAGCTGTTGGAGACAAACCGGCGAGAAACATCCCGATTGACAGCAAC 240
DB 757 CTAAACGAGAGCTAATGGAGCAGAACGACTGAGAAATGTGACGCGCTGTGCGGAAC 816

QY 241 CAGCAGTTCCTTATCGCAGGCTCATCTGTTACGAGACGAGCGGTGACGAGCGCTTCTGAT 300
DB 817 CAGCAGTTCCTTATCGCAGGCTCATCTGTTACGAGACGAGCGGTGACGAGCGCTTCTGAT 876

QY 301 GAAGATTGAGAGGATTAACGAGAGTTCAGGAGCGGACGAGCGGATGAAACGAGAGTCT 360
DB 877 GAAGATTGAGAGGATTAACGAGAGTTCAGGAGCGGACGAGCGGATGAAACGAGAGTCT 936

QY 361 GACACTCCCTTCGCGCAGATCAAGAGGATTCAGGAGCGGATGAAACGAGAGTCT 420
DB 937 GACACTCCCTTCGCGCAGATCAAGAGGATTCAGGAGCGGATGAAACGAGAGTCT 996

QY 421 TTGCGAAGGAGTTCGCGCAGGTTTGGCAAGATCTGCGAGCGGTGACGAGCGCTTCTGAT 480
DB 997 TTGCGAAGGAGTTCGCGCAGGTTTGGCAAGATCTGCGAGCGGTGACGAGCGCTTCTGAT 1056

QY 481 AAGGCTTGTCTAAGTGAAGTAAATGATGCTTCGAGTTCGCGCAGATCAAGTTCGCGCTCA 540
DB 1057 AAGGCTTGTCTAAGTGAAGTAAATGATGCTTCGAGTTCGCGCAGATCAAGTTCGCGCTCA 1116

QY 541 GACAGTGTCTGTTTGGCGAACAACGAGGATTCAGGAGCGGATGAAACGAGAGTCT 600
DB 1117 GACAGTGTCTGTTTGGCGAACAACGAGGATTCAGGAGCGGATGAAACGAGAGTCT 660

QY 601 ATGCGCTTACGATCGAGGATCTTACGCACTTCTGCGCGGTGATGATCTTCTGCGGTG 660
DB 1177 ATGCGCTTACGATCGAGGATCTTACGCACTTCTGCGCGGTGATGATCTTCTGCGGTG 1236

QY 661 GACAACTCCATTAAGCGCTGCTCAGCGTGTGTCATCTTCTGCGCGGTGATGATCTTCTGCGGTG 720
DB 1237 GACAACTCCATTAAGCGCTGCTCAGCGTGTGTCATCTTCTGCGCGGTGATGATCTTCTGCGGTG 780

QY 721 GAGCAGCGGCAACTGTTGGAGAAATCCAGCGGTGATCTGCGAGTTCAGGATCGCTCCGATCTAT 780
DB 1297 GAGCAGCGGCAACTGTTGGAGAAATCCAGCGGTGATCTGCGAGTTCAGGATCGCTCCGATCTAT 1356

QY 781 ATCTGAAACGAGTGAAGCGGTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 1357 ATCTGAAACGAGTGAAGCGGTGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1416

QY 841 ATCTCTCTGAGCTACGAGCTGCGGATGCAAACTCCAAACATGTCATCTTCTGCGGTGCTGCTGCTGCT 900
DB 1417 ATCTCTCTGAGCTACGAGCTGCGGATGCAAACTCCAAACATGTCATCTTCTGCGGTGCTGCTGCTGCTGCT 948

QY 901 CTCAGAAACGAGAGCTGCGCGCTTCTCTGAGGAGATCTGCGGTG 948
DB 1477 CTCAGAAACGAGAGCTGCGCGCTTCTCTGAGGAGATCTGCGGTG 1524

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RESULT 5  
US-10-087-167-136

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; Sequence 136, Application US/10087167
; Patent No. 6958236
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 136
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1863)
; OTHER INFORMATION: Ecdysone receptor chimera G(M)MD
; US-10-087-167-136

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Query Match      58.6%; Score 617.4; DB 3; Length 1863;
Best Local Similarity 76.3%; Pred. No. 1.7e-167;
Matches 759; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

QY 1 CCTGAGTGGTGTAGTACCCGAGACTCAGTGGCCATGAGCGGAAAGAGAGAAAGCAG 60
DB 577 CCGAGTGGTGTGTCCAGAGTCCAGTGCAGAGACAAAGAAAGAAAGAAAGCAG 636

QY 61 AAGGAGAGGACAACTGCTGTGACGACGAGCGGTGACGACCAATGCGGCCATT 120
DB 637 AGAGAAAGACAACTGCGAGTCACTGACGACGAGCGGTGACGACCAATGCGGCCATT 696

QY 121 ATGCAATGTGAACCTTCCACTCTGTAAGCAGCAAGGATTCAGAAAGTGTGTCAGAGTTT 180
DB 697 ATGCAATGTGAACCTTCCCGCCCCAGAGCGGCAAGGATTCAGAAAGTGTGTCAGAGTTT 756

QY 181 CTCTCCGACAAAGCTGTTGGAGCAGAACCGGCGAGAAACATCCCGATTGACAGCAAC 240
DB 757 CTAAACGAGAGCTAATGGAGCAGAACGACTGAGAAATGTGACGCGCTGTGCGGAAC 816

QY 241 CAGCAGTTCCTTATCGCAGGCTCATCTGTTACGAGACGAGCGGTGACGAGCGCTTCTGAT 300
DB 817 CAGCAGTTCCTTATCGCAGGCTCATCTGTTACGAGACGAGCGGTGACGAGCGCTTCTGAT 876

QY 301 GAAGATTGAGAGGATTAACGAGAGTTCAGGAGCGGACGAGCGGATGAAACGAGAGTCT 360
DB 877 GAAGATTGAGAGGATTAACGAGAGTTCAGGAGCGGACGAGCGGATGAAACGAGAGTCT 936

QY 361 GACACTCCCTTCGCGCAGATCAAGAGGATTCAGGAGCGGATGAAACGAGAGTCT 420
DB 937 GACACTCCCTTCGCGCAGATCAAGAGGATTCAGGAGCGGATGAAACGAGAGTCT 996

QY 421 TTGCGAAGGAGTTCGCGCAGGTTTGGCAAGATCTGCGAGCGGTGACGAGCGCTTCTGAT 480
DB 997 TTGCGAAGGAGTTCGCGCAGGTTTGGCAAGATCTGCGAGCGGTGACGAGCGCTTCTGAT 1056

QY 481 AAGGCTTGTCTAAGTGAAGTAAATGATGCTTCGAGTTCGCGCAGATCAAGTTCGCGCTCA 540
DB 1057 AAGGCTTGTCTAAGTGAAGTAAATGATGCTTCGAGTTCGCGCAGATCAAGTTCGCGCTCA 1116

QY 541 GACAGTGTCTGTTTGGCGAACAACGAGGATTCAGGAGCGGATGAAACGAGAGTCT 600
DB 1117 GACAGTGTCTGTTTGGCGAACAACGAGGATTCAGGAGCGGATGAAACGAGAGTCT 660

QY 601 ATGCGCTTACGATCGAGGATCTTACGCACTTCTGCGCGGTGATGATCTTCTGCGGTG 660
DB 1177 ATGCGCTTACGATCGAGGATCTTACGCACTTCTGCGCGGTGATGATCTTCTGCGGTG 1236

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Db 550 CCCCCTCCACCGCCAAACAGCAGTTCCTGATCCGAGGCTGGTGGTATCCAGGACGGATAC 609
Qy 286 GAGCAGCGCTTCTGATGAAGATTTGAAGAGGATTAACGACAGCTGGCGCAGCAAGCGACGAT 345
Db 610 GAGCAGCGCTTCCGGAAGAGATCTCAAAAGGTTGACGAGACTTGGCAATCAGCAGATGAA 669
Qy 346 GAAACGAGAGTCTGACATCCCTTCGCGCAGATCAAGAGATGATATCTCTCACGGTC 405
Db 670 GAAGCAGAGACTCAGACATGCCATTCGCGCAGATCAAGAAATGACCATCTCACAGTA 729
Qy 406 CAACCTATCTGGAGTTCCGCGAGGATTCGCGGTTCCAGAGATCTCGCAGCTGAT 465
Db 730 CAGCTAATAGTCGAGTTTCCCAAAGGCTACCTCGTTTTCAAAGATCTCACACCTGAC 789
Qy 466 CAAATTAACGCTGCTTAAGGCTTGTCAAGTGAGGTAATGATGCTCCGAGTCCGCGCAGCA 525
Db 790 CAGATCACAATTAAGGCAATGCTCAAGCGAAGTATGATGCTCGAGTAGCGAGCGG 849
Qy 526 TAGCATCGGCTCAGACAGTGTCTGTTCCGCGAACAACCAAGCGTACACTCGCGCAAC 585
Db 850 TACGACGCGGTGTCGATAGCGTTCTGTTCCCAAACCAACAGCGGTACACTCGCGCAAC 909
Qy 586 TACGCGAAGGCTGCATGGCTACGTCATCAGAGATCTACGCACTTCTCGCGGTGCATG 645
Db 910 TACGCGAAGGCGGCATGGGCTACGTCATCGAAGACCTGCTGCACTTCTCGCGGTGCATG 969
Qy 646 TACTCTATGGCGTTGGACAACATCCATTAAGCGCTGCTCAGCGGTGTCGTCATCTTTTCT 705
Db 970 TACTCGATGTCGATGGAACAGTGCATTAAGCGCTCTCTACTGCACTGTTATATTCG 1029
Qy 706 GACCGCGCAGGTTGGAGCAGCCGCAACTGTTGGAAGAAATCCAGCGGTACTACTGCAAT 765
Db 1030 GATCGCGCGGCTTAGAGCAGCCACAGCTAGTAGAAGAGATCCAGCGGTATTACTTGAAC 1089
Qy 766 ACCTCCGCACTATATCTTGAACAGCTAGCGGTCGCGGCTTCTCGCTCATATAC 825
Db 1090 ACCTGCGGCGGTATCATATGAACAGCAGCAGCGCGTTCGCGGCTTCTCGCGCTCATCTAC 1149
Qy 826 GCGAAGATCTCTCAATCTCTGAGTACGACGCTGCGCATGCAAAATCTCAACATG 885
Db 1150 GCGAAGATCTCTCGGTGCTTACCGATTCGCGAGCTGGCGATGCAAGATTCGAATG 1209
Qy 886 TGCACTCTCCCTCAAGCTCAAGAACAGAAAGCTGCGCGCTTCTCTCGAGGAGATCTGGGAT 945
Db 1210 TGCACTCTCGTGAAGCTCAAGAACAGGAGCTGCGCGCTTCTCTGAGGAGATCTGGGAC 1269
Qy 946 GTG 948
Db 1270 GTG 1272

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RESULT 12

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US-10-087-167-124
; Sequence 124, Application US/10087167
; Patent No. 6958236
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1782
; TYPE: DNA

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; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1782)
; OTHER INFORMATION: Ecdysone receptor chimera G(B)EV
US-10-087-167-124

Query Match      58.3%; Score 614.2; DB 3; Length 1782;
Best Local Similarity 78.4%; Pred. No. 1.4e-166;
Matches 755; Conservative 0; Mismatches 193; Indels 15; Gaps 1;

Qy 1 CTTGAGTGGTAGTACCCGAGACTCGATGGCCCATGAGCGGGAAGAGAGAGACAG 60
Db 577 CCCGAGTGGTGGTGGCGAGAAACGCGAGTGTGCGCAAAAGGAAAGAGAAAGCAG 636
Qy 61 AAGGAGAGAGACAAAATGCTCTGTGACGACGACGCGTGGACACACACATCGCCCAAT 120
Db 637 AGAGAAAGAGACAAAATGACGAGTGGACACACGACGAGTAGACGATCATATGCCCCATC 696
Qy 121 ATGCAGTGGAACCTCCACTCTCTGAAAGCAGCAAGGATT-----CAGGAA 165
Db 697 ATGCAGTGTGATCCACCAACCCCGAGGAGCGAGGATTCTGGAATGTTTGCAGCATGAA 756
Qy 166 GTGGTCCCAAGGTTTCTCTCGACACAGCTGTTGGAGACAAACCGGACAGAAACATCCCC 225
Db 757 GTGGTCCCGCGGTTCTCTCTCGGAGAGCTGATGGAGCAAAATCGGCTGAAGAAACATACC 816
Qy 226 CAGTGTACAGCCAAACAGACAGTTCCTTATCGCCAGGCTCATCTGTTACAGGACGGGTAC 285
Db 817 CCCTCAGCCGCAACACAGCAGTTCCTGNTCGGAGGCTGGTGTGGTACAGAGCGGATAC 876
Qy 286 GAGCAGCCTTCTGATGAAGATTTGAAGAGGATTTACGACAGCGTGGCAGCAAGCGGACGAT 345
Db 877 GAGCAGCCTTCCGAGAGAGATCTCAAAAGGCTGACGAGACTTTGGCAATCAGCAGATGAA 936
Qy 346 GAAAGCAGAGAGTCTGACATCTCCCTCCGCGCAGATCAGAGATGATATCTCTCAGCGTC 405
Db 937 GAAGCAGAGAGCTCAGACATGCCATTTCCGCGCAGATCAGAGAAATGACCATCTCTCACAGTA 996
Qy 406 CAACTTATGTTGAGTTCGGAAGGATTCGCAAGGTTCCGCAAGATCTCGCAGACCTGAT 465
Db 997 CAGCTAATAGTCGAGTTTCCAAAGGCTTACCTGGTTTTTCAAAGATCTCAACACCTGAC 1056
Qy 466 CAAATTAACGCTTAAAGGCTTCTCTCAAGTGAAGTAAATGATGCTCCGAGTCCGCGCAGCA 525
Db 1057 CAGATCACAATTTAAGGCATGCTCAAGCGAAGTATGATGCTGCGAGTAGCGAGGCG 1116
Qy 526 TAGATGCGGCTCAGACAGTGTCTGTTCCGCGAACAACCAAGGCTACACTCGCGGACAC 585
Db 1117 TACGACGCGGTGTCGATAGCGTTCTGTTCCGCAACCAACAGCGGTACACTCGCGACAC 1176
Qy 586 TACCGCAAGGCTGGCATGGCTACGTCAGGAGTCTACTGCACATTCTGCGCGTGCATG 645
Db 1177 TACCGCAAGGCGGCATGGCTTACGTCATCGAAGACCTGCTGCACATTCTGCGCGTGCATG 1236
Qy 646 TACTCTATGGCGTTGGACAAACATCCATTACGCGCTGCTCACGCTGCTCGTCATCTTTCT 705
Db 1237 TACTCGATGTCGATGACAAAGTGCATTAGCGCTCTCTCACTGCCATCGTTATATCTCG 1296
Qy 706 GACCGCCAGGTTGGAGCAGCGCAACTGGTGGGAAGAAATCCAGCGGTACTACTGGAAT 765
Db 1297 GATCGGCGGCGCTAGAGCAGGCCACAGCTAGTAGAAGAGATCCAGCGGTATTACTCTGAAC 1356
Qy 766 ACCTCGCATCTATATCTTGACACAGCTGAGCGGTGCGCGGTTCGTCGTCATATAC 825
Db 1357 ACCTCGCGGTGATCATCATGAACACGACAGCGGTGCGCGGTTCGCGCGTCTATC 1416
Qy 826 GCGAAGATCTCTCAATCTCTCTGAGCTACGACGCTCGGATGCAAAATCTCAACATG 885
Db 1417 GCGAAGATCTCTCGGTGCTTACCGAGTTGCGGACGCTGGGATGCAAGATTCGAACATG 1476
Qy 886 TGCACTCTCCCTCAAGCTCAAGAACAGAAAGCTGCGCGCTTCTCTGAGGAGATCTCGGAT 945

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Db 1477 TGCATCTCGTGAAGCTCAAGAACAGGAAGCTGCGCGCTTCTCTGGAGGAGATCTGGGAC 1536

Qy 946 GTG 948  
|||

Db 1537 GTG 1539

RESULT 13  
US-10-087-167-65  
; Sequence 65, Application US/10087167  
; Patent No. 6958236  
; GENERAL INFORMATION:  
; APPLICANT: Pascal, Erica  
; APPLICANT: Valentine, Scott  
; APPLICANT: Brown, Jeffrey  
; APPLICANT: Cockrell, Adam  
; APPLICANT: Johnson, Brian  
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS  
; FILE REFERENCE: 50018A  
; CURRENT APPLICATION NUMBER: US/10/087,167  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 60/242,969  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 65  
; LENGTH: 1509  
; TYPE: DNA  
; ORGANISM: Synthetic construct  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1509)  
; OTHER INFORMATION: Ecdysone Receptor chimera MBV  
US-10-087-167-65

Query Match 58.0%; Score 611.4; DB 3; Length 1509;  
Best Local Similarity 78.5%; Pred. No. 8.5e-166;  
Matches 745; Conservative 0; Mismatches 201; Indels 3; Gaps 1;

Qy 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCGCATGAGCGGAAAGAGAAAGACACAG 60  
Db 310 CCGAGTGGCTGGTCCGAGAGTCCACGTCCAGAAACAAAGAAAGAAAGAAAGACAG 369

Qy 61 AAGGAGAGGACAAATCTGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 120  
Db 370 AGAGAAAAGACAAATCTGTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 429

Qy 121 ATGCAAGTGTGAACCTCCACCTCTCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 180  
Db 430 ATGCAAGTGTGAACCTCCGCGCCGAGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTTC 489

Qy 181 CTCTCCGACAGCTGTTGGAGACAAACCGGACAGAAACATCCCCAGTTTGACAGCAGCAGC 240  
Db 490 CTAACGGAGAGAGCTAATGGAGCAGAAACAGACTGAAGAAATGTGAGCGCGCTGTGGCGAAC 549

Qy 241 CAGCAGTTCTTATGCGCAGGCTCATCTGTACAGAGCGGTACGAGCAGCCTTCTGAT 300  
Db 550 CAGAACTCCCTGATTCGGGAGGCTCGTGTGTGTACAGGAGGCTATGAAACAACTTCAGAG 609

Qy 301 GAAGATTTGAAGAGATTTACGACAGCTGGCAGCAAGCGAGATGAAAGAGAGCTCT 360  
Db 610 GAAGATTTGAAGAGATTTACGACAGCTGGCAGCAAGCGAGATGAAAGAGAGCTCT 666

Qy 361 GACATCTCTCCGCGCAGATCAGAGATGACTATCTCTCAGGTCCTCACTTATCGTGGAG 420  
Db 667 GATATGCGTTTCCGCGCAGATCAGCAGATGAGATCTGACAGTTCAACTCATGTTAGAA 726

Qy 421 TTCCGAGAGGATTTGCCAGGGTTGCCAGATCTCGCAGCAGCTGATCAAAATACGCTGCTT 480  
Db 727 TTCCGAGAGGATTTGCCAGGGTTGCCAGATCTCGCAGCAGCTGATCAAAATACGCTGCTT 786

Qy 481 AAGGCTTGTCTCAAGTGAAGTAAATGATCTCTCGAGTCCGCGAGCAGATGAGTGGCGCTCA 540  
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Db 787 AAGGCGTGTTCAGGTGAGTGATGCTCTCGAGTGGCGCGGTACGACGCGGCCACC 846

Qy 541 GACAGTGTCTTCTGTCGCGAAACAAACGAGTACACTCGGGAACAACCTACCGAAGGCTGGC 600  
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Db 847 GACAGGTAATCTGTCGCGAAACAAACGAGGCTACTCCGCGACAACCTACCGAAGGCGAGC 906

Qy 601 ATGGCTTACGTCATCGAGGATCTACTGACACTTCTGCGGTGATGATCTCTATGGGTTG 660  
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Db 907 ATGTCTTACGTCATCGAGGATCTCTTGCACATCTCTGCGGTGATGATCTCTATGATGATG 966

Qy 661 GACAAATCCATTAAGCGCTGCTCAGCGGTGCTGCTCTTTCTGACCGGCGCAGGTTG 720  
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Db 967 GATAAGTGCATCTACGCGCTGCTTACGGCCATGTCATTTCTCAGACGCGCTGGGCTC 1026

Qy 721 GAGCAGCGCAACTGCTGGAAGAAATCCAGCGGTACTACTGAATACGCTCCGATCTAT 780  
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Db 1027 GAGCAACCTTATGCTGGAAGAAATCCAGCGGTATTAACCTGAACACGCTGGGCGGTATC 1086

Qy 781 ATCTGAAACCAAGCTGAGCGGTGCGCGGTGCTGCTCGGTATATAGCGCAAGATCTCTCA 840  
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Db 1087 ATCTGAAACCAAGCTGAGCGGTGCGCGGTGCTGCTCGGTATATAGCGCAAGATCTCTCA 1146

Qy 841 ATCTGAGTACGACGCTCGGCAATGCAAACTCCAAATGTCATCTCCCTCAAG 900  
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Db 1147 ATATTGACGAGCTGCGGACCTCGGATGCGAGACTCCAAATGTCATCTCTGTTGAAG 1206

Qy 901 CTCAAGACAGAAAGCTGCGCGCTTCTCTCGAGGAGATCTGGGATGG 949  
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Db 1207 CTGAAGATAGGAAGCTGCGCGCTTCTCTCGAGGAGATCTGGGAGCTGG 1255

RESULT 14  
US-10-087-167-118  
; Sequence 118, Application US/10087167  
; Patent No. 6958236  
; GENERAL INFORMATION:  
; APPLICANT: Pascal, Erica  
; APPLICANT: Valentine, Scott  
; APPLICANT: Brown, Jeffrey  
; APPLICANT: Cockrell, Adam  
; APPLICANT: Johnson, Brian  
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS  
; FILE REFERENCE: 50018A  
; CURRENT APPLICATION NUMBER: US/10/087,167  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 60/242,969  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 118  
; LENGTH: 1776  
; TYPE: DNA  
; ORGANISM: Synthetic Construct  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1776)  
; OTHER INFORMATION: Ecdysone receptor chimera G(M)BV  
US-10-087-167-118

Query Match 58.0%; Score 611.4; DB 3; Length 1776;  
Best Local Similarity 78.5%; Pred. No. 9.1e-166;  
Matches 745; Conservative 0; Mismatches 201; Indels 3; Gaps 1;

Qy 1 CTTGAGTGGCTAGTACCCGAGACTCAGTGGCGCATGAGCGGAAAGAGAAAGACACAG 60  
Db 577 CCGAGTGGCTGGTCCGAGAGTCCAGTCCAGAAACAAAGAAAGAGAAAGAGACAG 636

Qy 61 AAGGAGAGGACAAATCTGCTGTGACGACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 120  
Db 637 AGAGAAAAGACAAATCTGCGAGTCACTGACGACAGTGGAGCAGTATGATGCTGCTGATA 696

Qy 121 ATGCAAGTGTGAACCTCCACCTCTCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 180  
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Db 697 ATGCAATGTGACCTCCGCCCCCAGAGCGGCGAAGGATTACAGAGTGGTCCGAGGTTTC 756  
Qy 181 CTCTCCGCAAGCTGTTGGAGACAACCGCGAGAAAAACATCCCCCGATTGACAGCCAAAC 240  
Db 757 CTAACGGAGAGCTAAATGGAGCAGAACAGACTGGAAGATGTGACCGCGCTGTGCGCGAAC 816  
Qy 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGGTACCAAGACGGGTACGAGCAGCTTCTGAT 300  
Db 817 CAGAAGTCCCTTGATCGCGAGGCTCGTGTGGTACCAAGGAGGCTATGAACAACCTTCTAGAG 876  
Qy 301 GAAGATTGGAAGAGATTACCGACAGCTGGCGAGCAAGCGGAGCATGAAGAAAGAGAGTCT 360  
Db 877 GAAGACCTCAGAGGGTGCAGCAGACCTGGCAG--TCGACAGAGATGAAGAGAGTCA 933  
Qy 361 GACACTCCCTCCCGCAGATCAGAGAGTACTATCTCCAGCGTCCAACTTATCTGTGAG 420  
Db 934 GATATGCGGTTCGCCAGATCACCGAGATGACGATCTCTGACAGTTCAACTCATCTGTAGAA 993  
Qy 421 TTCGGAAGGATTGCCAGGCTTCCGCAAGATCTCGCAGCTGTATCAAAATTACGCTGTT 480  
Db 994 TTCGCAAAAGGCTTCCCAAGGCTTCCCAAGATCTCGCAGTCCGATCAAAATCACGTTACTA 1053  
Qy 481 AAGCTTCTCAAGTGAAGTAAATGATCTCCGAGTCCGCGACGATACGATCGCGGCTCA 540  
Db 1054 AAGCGGTGTTCAAGTGAAGTAAATGATCTCCGAGTCCGCGGCGGATGACGCGCGCCACC 1113  
Qy 541 GACAGTGTCTTTCGCGAAACAACAGCGTACACTCGCGCAAACTACCGCAAGGCTGGC 600  
Db 1114 GACAGCGTACTGTTCCGCCAACCAACAGCGGTACTCCCGCGACAACTACCGCAAGCGAGGC 1173  
Qy 601 ATGCGCTACGTCAGGAGTCTACTGCACTTCTCGCGGTGTCATGTACTCTATGCGGTG 660  
Db 1174 ATGTCCTACGTCATCGAGGATCTCTTGCACTTCTGTGCGTGCATGTACTCTCATGATG 1233  
Qy 661 GACAACATCCATTACGCGTCTCAAGCGTCTGCTGCTGCTATCTTCTGACCGGCGGTTG 720  
Db 1234 GATTAAGTGCACTACGCGCTCTTACGCGCATGTCTATTTCTCAGACCGGCTTGGGCTC 1293  
Qy 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACCTGAATAGCTCCGCACTAT 780  
Db 1294 GAGCAACCTTATTGTTGGAAGAAATCCAGCGGTATTACCTGAACACGCTGCGGGTGTAC 1353  
Qy 781 ATCTGAACAGCTGAGCGGTGCGCGGTGCTGCTCGCTCATATATACGGAAGATCCTCTCA 840  
Db 1354 ATCTTGAACCAAAACAGTGCCTGCGCGCTGCGCGGTAGTCTTTCGCAAGATCCTGGGG 1413  
Qy 841 ATCTCTCTGAGCTACGCAAGCTCGGCATGCAAACTCCCAAGTGCATCTCCCTCAAG 900  
Db 1414 ATATTGCGGAGCTGCGGACCTCGGCATGCAAGATCCAAATGTGATCTCGTTGAAG 1473  
Qy 901 CTCAGAACAGAAAGCTGCGGCTTCTCTCGAGGAGATCTGGGATGTGG 949  
Db 1474 CTGAAGATAGGAGCTGCGCGCTTCTCTCGAGGAGATCTGGGAGTGG 1522

## RESULT 15

US-10-087-167-79  
; Sequence 79, Application US/10087167  
; Patent No. 6958236  
; GENERAL INFORMATION:  
; APPLICANT: Pascal, Erica  
; APPLICANT: Valentine, Scott  
; APPLICANT: Brown, Jeffrey  
; APPLICANT: Cockrell, Adam  
; APPLICANT: Johnson, Brian  
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS  
; FILE REFERENCE: 50018A  
; CURRENT APPLICATION NUMBER: US/10/087,167  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 60/242,969  
; PRIOR FILING DATE: 2000-10-24  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 79  
; LENGTH: 1533  
; TYPE: DNA  
; ORGANISM: Synthetic construct  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1533)  
; OTHER INFORMATION: Ecdysone Receptor chimera EMV  
US-10-087-167-79

Query Match 57.8%; Score 609.6; DB 3; Length 1533;  
Best Local Similarity 75.7%; Pred. No. 2.8e-165;  
Matches 775; Conservative 0; Mismatches 234; Indels 15; Gaps 1;

Qy 1 CCTGAGTGCCTAGTACCCGAGACTCAAGTGCCTCAAGCGGAAAGAGAAAGACACAG 60  
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Qy 61 AAGGAGAGAGACAAACTGCTCTGTCAGCAGCAGCGGTGACACACATGCGCCCATTT 120  
Db 370 AGAGAAAAAGACAAACTTACCAGTGAGCAACACGACAGTAGACGATCATATGCCCCCAATC 429  
Qy 121 ATCAGTGTGAACCTCCACCTCTGAGAGCAGCAAGGATT-----CAGGAA 165  
Db 430 ATGCAAGTGTATCCACCACCCCGAGGAGCGAGGATTCTGGAATGTTTGCAGCATGAA 489  
Qy 166 GTGCTCCCAAGGTTTCTCTCCGACAAAGCTGTTGGAGACAAACCGGAGAAAGAAACATCCCC 225  
Db 490 GTGCTCCCGCGGTTCTCTCGGAGAGCTGATGGAGCAGATCGGCTGAAGACATATACC 549  
Qy 226 CAGTTGACAGCAACCAAGCAGTTCCTTATGCGCAGGCTCATCTGGTACCAAGACGGGTAC 285  
Db 550 CCCTTCAACCCCAACCAAGCAGTTCCTGATCGCAGGCTGGTGTGCTACCAAGAGGGGTAC 609  
Qy 286 GAGCAGCTTCTGATGAAGATTGGAAGAGATTACGACAGCTGGCAGCAAGCGGACGAT 345  
Db 610 GAGCAGCGCTCGGAGAGATCTCAAGAGAGTTACACAGACATGGCGATTTAGAAAGAA 669  
Qy 346 GAAAAAGAGAGTCTGACACTCCCTTCCGACAGATCACAGAGATGACTATCTCACCGTTC 405  
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Qy 406 CAATTTATCTGAGTTCGCAAGGATTCGCAAGGTTTCGCAAGATCTCGCAGCTGAT 465  
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Qy 466 CAATTTACGCTGTTAAGGCTTCTCAAGTGAAGTAAATGATGCTCCGAGTCCGCGACGA 525  
Db 790 CAATTTACATTTAAGGGGCTCATCAAGCGAAGTGAATGCTGCGAGTGGCGGACGG 849  
Qy 526 TACGATGCGGCTTCAGACAGTGTCTGTTCCGCAACAAACCAAGCTACACTCCGCGAAC 585  
Db 850 TACGACGCGGAGCGACAGCGTGTCTGTCGCAACCAACCAAGGCTACACGCGGACAC 909  
Qy 586 TACGCAAGGCTCGCATGCGCTTACGATGAGGATCTACTGCACTTCTGCGCGGTGATG 645  
Db 910 TACCGCAAGCGGCGCATGTCTACGTCATCGAGGACCTGCTGCACTTCTGCTCGGTGATG 969  
Qy 646 TACTCTATGCGGTGGACACATCCATTAAGCGCTGCTCAGCGCTGCTGCTCATCTTTTCT 705  
Db 970 TACTCCATGAGCATGGAACAATGTGCACTAGCGCTGCTCAGCGCCATCGGTATATTCTCA 1029  
Qy 706 GACCGCGCAGGGTGGAGCAGCGCAACTGTTGGAAAGAAATCCAGCGGTACTACCTGAAT 765  
Db 1030 GACCGCGCAGGCTCGAGCAGCAACCCCTTTTAGTGGAGAAATCCAGAGATACTACTGAAG 1089  
Qy 766 ACCTCCGCACTTATATCTTGAACAGCTGAGCGGTCGCGCGTTCGTCGCTCATATAC 825  
Db 1090 ACCTGCGGGTTTACATTTTAAATCAGCAGCGCTGCGCTGCTGCGCGGTGCTTTC 1149  
Qy 826 GGCAAGATCTCTCAATCTCTCTGAGCTTACGACGCTCGGCGATGCAAACTCAACATG 885  
Db 1150 GGCAAGATCTCTGCGCGTGTGACGGAACCTGCGACGCTCGGCAAGCTCAACATG 1209

Qy	886	TGCATCTCCCTCAAGCTCAAGAACAGAAAGCTGCGGCTTTCTCGAGGAGATCTGGAT	945
Db	1210	TGCATCTCGCTGAGCTGAAGAACAGAAACTTCCGCCATTCCTCGAGGAGATCTGGAC	1269
Qy	946	GTGGCGGACATGTGCAACACCCACCGCGCTATCCTCGAGTCCCCCAGAAATCTCTAG	1005
Db	1270	GTGGCGAAGTGTGACGACGAGCTTGCCCCCGGACCGATGTCAGCCTGGGGGACGAG	1329
Qy	1006	CCCC	1009
Db	1330	CTCC	1333

Search completed: January 31, 2006, 14:11:00  
Job time : 236 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2006, 09:09:55 ; Search time 4078 Seconds  
(without alignments)

12092.591 Million cell updates/sec

Title: US-09-965-703A-3

Perfect score: 1054

Sequence: 1 cctgagtcgtagtaccgca.....gtccggccgcgtctctga 1054

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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EST:\*

1: gb\_est1.\*

2: gb\_est2.\*

3: gb\_est3.\*

4: gb\_est4.\*

5: gb\_est5.\*

6: gb\_est6.\*

7: gb\_est7.\*

8: gb\_est8.\*

9: gb\_est9.\*

10: gb\_est10.\*

11: gb\_est11.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	314.2	29.8	963	CNS0905M	BX067382 Single re
2	233.6	24.1	728	BM650826	BM650826 17000873
3	231.4	22.0	851	CNS011ME	AL100448 Drosophila
4	200.8	19.1	470	AA538642	AA538642 LD18219.5
5	151.6	14.4	574	AI258616	AI258616 LP01848.5
6	146.2	13.9	1050	CNS016VX	AL107379 Drosophila
7	130	12.3	1088	BM650826	BX463524 BX463524
8	127.6	12.1	867	BQ222200	BQ222200 AGENCOURT
9	127	12.0	1031	BQ058428	BQ058428 AGENCOURT
10	125.6	11.9	1963	AK077620	AK077620 Mus muscu
11	125.4	11.9	651	CN309352	CN309352 170005999
12	125.4	11.9	667	CD673041	CD673041 fg19g05.Y
13	125.4	11.9	918	BQ214241	BQ214241 AGENCOURT
14	125.4	11.9	1386	DQ052757	DQ052757 Homo sapi
15	125.4	11.9	1685	CR614375	CR614375 full-leng
16	125.4	11.9	1763	CR610600	CR610600 full-leng
17	125.4	11.9	1828	CR617823	CR617823 full-leng
18	125.4	11.9	1922	CR604070	CR604070 full-leng
19	125.4	11.9	1924	CR609885	CR609885 full-leng
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# ALIGNMENTS

RESULT 1  
CNS0905M

LOCUS

DEFINITION

Single read from an extremity of a full-length cDNA clone made from

Anopheles gambiae total adult females. 5-PRIME end of clone

PK0AAC51AC03 of strain 6-9 of Anopheles gambiae (African malaria

mosquito).

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

PubMed

Reference

Authors

Title

Journal

PubMed

Reference

Authors

Title

Journal

PubMed

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Authors

Db 9 GAAATCCACTTCGCGCACAATACGAAATCACCATCTCCACAGTACACAACTAATCGTCGAG 68  
 QY 421 TTCCGGAAGGGATTGCGAGGGTTGCGCAAGATCTCCGAGCTGATCAAAATACGCTGCTT 480  
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 QY 481 AAGGCTTGCTCAAGTAGGTAATGATGCTCCGAGTCCGCGAGTACGATGCGGCTCA 540  
 Db 128 AAGGCTTGCTCCAGTAGGTAATGATGCTCCGAGTCCGCGAGTACGATGCGGCTCA 187  
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 QY 661 GACAACATCATTAGCGGCTGCTCAGCGTGTGTCATCTTTTCTGACCGCGCAGGTTG 720  
 Db 308 GACAGCTGAGTACGCGCTGCTGACCGGATCGTCACTTCTCCGACCGCGCGGCTC 367  
 QY 721 GAGCAGCGCAACTGTGTGAAGAAATCCAGCGGTACTTACCTGAATAGCTCCGCACTAT 780  
 Db 368 GAGAGCGCGAGCTGTGTGAACGATCCAGAGCTACTTACATCGACAGCTGCGGCTTAC 427  
 QY 781 ATCTGAAACAGCTGAGCGGTTGCGCGGTTGCTGCGTATATACGCGAAGATCCTCTCA 840  
 Db 428 ATCTGAAACAGCTGAGCGGTTGCGCGGTTGCTGCGTATATACGCGAAGATCCTCTCA 885  
 QY 841 ATCTCTCTGAGCTACGACGCTGCGCATCGCAATCCAAATCTCCAAATGTGCACTCCCTCAAG 900  
 Db 486 ATCTGACCGAGCTGCGGAGCGCTGCGCAACGAGACTCGGAGATGTGCTTCTCGCTCAAG 545  
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 QY 961 C 961  
 Db 606 C 606

RESULT 2  
 BM650826 728 bp mRNA linear EST 26-FEB-2002  
 LOCUS 1700687372602 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
 DEFINITION 19600449637314 5', mRNA sequence.

ACCESSION BM650826  
 VERSION BM650826.1 GI:18950337  
 KEYWORDS EST.  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;  
 Culicidae; Anophelinae; Anopheles.

1 (bases 1 to 728)  
 Author: R.A., Lin J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,  
 Holt, R.A., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
 Celera Anopheles gambiae EST project  
 Unpublished (2002)  
 Contact: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr.,  
 Rockville, MD 20850, USA

Tel: 240453151  
 Fax: 2404534580  
 Email: holtra@celera.com  
 Plate: N001004AT row: E column: 24  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
 1. 728  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"

FEATURES  
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 /mol\_type="mRNA"

/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="19600449637314"  
 /dev\_stage="Adult"  
 /lab\_host="DH10b"  
 /clone\_lib="A.Gam.ad.cDNA1"  
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

ORIGIN

Query Match 24.1%; Score 253.6; DB 3; Length 728;  
 Best Local Similarity 66.3%; Pred. No. 3.2e-58;  
 Matches 418; Conservative 0; Mismatches 194; Indels 18; Gaps 3;  
 QY 1 CTTGAGTGGTAGTACCGAGACTCAGTCCGCGCATGAGCGGAAGAGAAAGACACAG 60  
 Db 105 CCGGAGTGGCTGCTGCGGAGAAATCAGTCCGCGCATCAGCGGAAGAGAAAGCGCGAG 164  
 QY 61 AAGGAGAAGGACAACTGCTCTGTCAGCAGCAGAC-----GTTGGACGACCATGTC 112  
 Db 165 AAGGAGAAGGACAACTGCTCCGCGCAACCGTGCACACCACCGTGAATGAAGAAACAGC 224  
 QY 113 CCGCCATTATGAGTGTGAACCTCCACCTCTCGAAGCAGCAAGGAT----TCACGAAGTG 168  
 Db 225 AGCAGCTACAAGTTCGAGCTGCTGCGGTGCTGATGAATGATCAACCGCCACCGCC 284  
 QY 169 GTCCCAAGTTTCTCTCCGACAAAGCTGTTGGAGACAAACCGGCGAGAAACATCCCCAG 228  
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 QY 229 TTGACAGCCAAACAGCAGTTCCTTATCGCGCAGCTCATCTGTTACCGAGCAGGTACGAG 288  
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 Db 405 CAACGTCGAGGAGAGATCTCAAGAGGATAATGATTAATCAACCCCAACGAGGAGGAGAT 464  
 QY 349 AAGGAAGTCTGACACTCCCTTCCGCGAGATCAGAGATGACTATCTCTCAGGTCGAA 408  
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 QY 409 CTTATCGTGGAGTTGCGGAAGGATGTCGAGGTTTCGCCAAGATCTCGCAGCCTGATCAA 468  
 Db 519 CTATCTCGAGTTTCGGAAGGAGATGTCGAGGATTTACCAAGATCCCGCAGGAGATCAG 578  
 QY 469 ATTACGCTCTTAAGGCTTGTCAAGTAGGAGTAATGATGCTCCGAGTCCGCGAGCATAC 528  
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 QY 589 CGCAAGGCTGGCATGGCTACGTCATCGAG 618  
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RESULT 3

CNS011ME

LOCUS

DEFINITION

Accession  
 Version  
 Keywords

CNS011ME 851 bp DNA linear GSS 26-JUL-1999  
 Drosophila melanogaster genome survey sequence SP6 end of BAC  
 BACN06K02 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 AL100448  
 AL100448.1 GI:5612059  
 GSS.

SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 851)
REFERENCE	Genoscope.
AUTHORS	Direct Submission
TITLE	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : <a href="mailto:secref@genoscope.cns.fr">secref@genoscope.cns.fr</a> - Web : <a href="http://www.genoscope.cns.fr">www.genoscope.cns.fr</a> )
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <a href="http://www.edgp.ebi.ac.uk">http://www.edgp.ebi.ac.uk</a> -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.
FEATURES	Location/Qualifiers
source	1..851 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" /clone="BACN06K02" /clone_lib="DrosBAC" /plasmid="pBelOBAC11" /note="end : Sp6"

ORIGIN	Query Match	22.0%	Score 231.4	DB 10	Length 851
	Best Local Similarity	65.9%	Pred. No. 4.2e-52		
	Matches 351	Conservative 0	Mismatches 181	Indels 1	Gaps 1
QY	478	CTTAAAGCCTTGCTCAACTGAGTGAATGATGCTCCGATCGGGCGACGATAGCATGCGGCC	537		
DB	262	CGTTAGGCCCTGCTCGTCGGAGGTGATGCTGCGTATGGCAGCAGCTATGACCACAGC	321		
QY	538	TCAGACAGTGTCTTGTTTCGGCGAACCAACAGCGTACACTCGCGACAACTACCGCAAGCCT	597		
DB	322	TCGGACTCAATATYCTTCGCGAATATAGATCATATACGGGGGATCTTTACAAATGCGCC	381		
QY	598	GGCATGCCCTPACGTCATCGAGGATCTACTGCACCTTCTGCCGGTGCACTGTACTCTATGCGG	657		
DB	382	GGAATGGCTGATAAATTTGAAGACCTGCTGCAATTTCTGCGGCCAAAATGTTCTCGATGAAG	441		
QY	658	TTGCGACAACTCCANTGACGGCTGCTCACGGCTGTGCTCATCTTTTCTGACCGGCCAGGG	717		
DB	442	GTGGACAACTCGGAATACGGCGCTTCTCACTGCCCATTTGTGATCTTCTCGGACCGGCCGCGG	501		
QY	718	TTGCGAGCAGCGCGAACTGGTGGGAAGAAATCCAGCGGTACTACCTGGAATACGCTCCGCAATC	777		
DB	502	CTGGAGAAGGCCCAACTAGTTCGAAGCGATCCAGAGCTACTACATCGACACGCTACGGATT	561		
QY	778	TATATCTGTAACAGCTGAGCGGGTGGCGGGTTGTCGCTGCATATATACGGCAAGATCCTC	837		
DB	562	TATATACTCAACCGCCCATCGCGGACTCAATGAGCCTT-CGTCTTTCTACGCCAAAGCTGCTC	620		
QY	838	TCAATCTCTCTCGAGCTACGCAGCTCGGCGATGCAAAACCTCCAACTATGTCATCTCCCTC	897		
DB	621	TCGATCTCTACCGAGCTTCGGTACGCTGGGCAACCGAAGCCGAGATGTGTCTTCTCACTA	680		
QY	898	AAGCTCAAGAACAGAAAGCTGCGCCCTTTCTCTCGAGGAGATCTGGGATGTGGCGGACATG	957		
DB	681	AAGCTCAAAACCGCAAACTGCCCAAGTTCTCTCGAGGAGATCTGGGAGCTTCATGCCATC	740		
QY	958	TCGCACACCCAAACCGCGCGCTATCTCTCGAGTCCCGCCACGGAATCTCTAGCCGCT	1010		
DB	741	CCGCGAATTCGGTTCAGTGCACCTTTAGATTACCCAGGAGGAGAACACGAGCGTCT	793		

RESULT 4  
AA538642

LOCUS	470 bp	mrna	linear	EST 19-APR-2001
DEFINITION	LD18219.5 prime 1D Drosophila melanogaster embryo BlueScript			
	Drosophila melanogaster cDNA clone LD18219 5prime similar to			
	M74078: Drosophila melanogaster ecdysone receptor (EcR) mRNA,			
	complete cds, mRNA sequence.			
ACCESSION	AA538642			
VERSION	AA538642.1	GI:2285158		
KEYWORDS	EST.			
SOURCE	Drosophila melanogaster (fruit fly)			
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
REFERENCE	1 (bases 1 to 470)			
AUTHORS	Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.			
TITLE	BDGP/HEMI Drosophila EST Project			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Stapleton, M. BDGP			
	Lawrence Berkeley National Lab			
	One Cyclotron Rd. Berkeley, CA 94720, USA			
	Fax: 510 486 6798			
	Email: <a href="http://www.fruitfly.org/EST">http://www.fruitfly.org/EST</a> , <a href="mailto:est@fruitfly.berkeley.edu">est@fruitfly.berkeley.edu</a>			
	Plate: 182 row: B column: 7			
	High quality sequence stop: 343.			
FEATURES	Location/Qualifiers			
source	1..470			
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	/mol_type="mRNA"			
	/db_xref="BDGP_EST:BDc1n017358"			
	/db_xref="taxon:7227"			
	/clone="LD18219"			
	/sex="male and female"			
	/dev_stage="0 to 24 hours mixed stage embryonic"			
	/lab_host="SOLR"			
	/clone_lib="LD Drosophila melanogaster embryo BlueScript"			
	/note="Organ: embryo; Vector: BlueScript SK; Site 1: EcRI; Site 2: XhoI; Constructed using Stratagene ZAP-cDNA Synthesis kit. Oligo dir-primed and directionally cloned at EcRI and XhoI in Bluescript SK(+/-)"			
ORIGIN				
Query Match	19.1%	Score 200.8;	DB 1;	Length 470;
Best Local Similarity	65.3%	Pred. No. 9.2e-44;		
Matches	295;	Conservative	0;	Mismatches 157;
			Indels	0;
			Gaps	0;
Qy	559	AACAACCAAGGTACACTCGCGCAAACTACCGCAAGGCTGGCATGGCTACGTATCGAG	618	
Db	1	AATAATAGATCATATACGCGGGATTCTTACAAAATGGCGGAATGGCTGATACATTGAA	60	
Qy	619	GATCTACTGCATCTTCGCGGTGCATGTACTCTATGCGGTGGACACATCCATTACGCG	678	
Db	61	GACCTGCTGATCTTCGCGCCCAATGTTCTCGAATGAAGGTGGCAACAGTCGATACGCG	120	
Qy	679	CTGCTCACGGCTGTCGTCATCTTTCTGACGGCGAGGTTGGAGCAGCGCGCACTGGT	738	
Db	121	CTTCTACTGCCATTGGATCTCTCGACCGCGCGGCTTGAGAGGGCTTAACCTAGTC	180	
Qy	739	GAAGAAATCCAGCGGTACTACCTGAATACGCTCCGCATCTATATCTCTGAAACCAAGCTGAGC	798	
Db	181	GAAGCATCCAGAGCTACTACATCGACACGCTACGCCATTTATATCTCAACCGCACTGC	240	
Qy	799	GGGTGCGCGGTTGCTCGTCATATACGGCAAGATCTCTCAATCTCTCTGAGCTACGC	858	
Db	241	GGCGACTCAATGAGCCTCTGCTTTCTAGCGAAAGCTGCTCTCGATCTCTCACCGAGCTCGT	300	
Qy	859	ACGCTGGCATGCAAACTCCAAATGTCATCTCCCTCAAGCTCAAGAACAGAAAGCTG	918	
Db	301	ACGCTGGCAACAGAACCGCGAGATGTGTTTCTCACTAAAGCTCAAAACCGCAACTG	360	
Qy	919	CCGCTTTTCTCGAGGAGATCTGGGATGTGGCGGACATGTTCGACACACCCAAACCGCGCCT	978	

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Db      361  CCNAGTTCCTCGAGGAGATCTGGAGCTTCATGCCATCCGCCATCGGTCCAGTCGCAC 420
QY      979  ATCTCGAGTCCCGCCAGATCTCTAGCCCT 1010
Db      421  CTTGAGATTACCCAGGAGGAGACGAGCGTCT 452

RESULT 5
AL258616
LOCUS   AL258616
DEFINITION
Drosophila melanogaster cDNA clone LP01848 5prime similar to
M74078; Ecr FBgn0000546 PID:9157318 SWISS-PROT:P34021, mRNA
sequence.
ACCESSION
AL258616
VERSION
AL258616.1 GI:3866141
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 574)
REFERENCE
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Teang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence DS05325
Plate: 18 row: D column: 12
High quality sequence stop: 533.
FEATURES
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/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="LP01848"
/sex="male and female"
/dev_stage="larvae-pupae"
/lab_host="DMS-alpha"
/clone_lib="LP Drosophila melanogaster larval-early pupal
pot2"
/notes="Organ: whole body; Vector: pot2; Site 1: EcoRI;
Site 2: XhoI; Sized fractionated cDNAs were directly
ligated into pot2. Plasmid cDNA library."

ORIGIN
Query Match 14.4%; Score 151.6; DB 1; Length 574;
Best Local Similarity 60.0%; Pred. No. 3.1e-30;
Matches 275; Conservative 0; Mismatches 174; Indels 9; Gaps 1;

QY      177  GTTTCCTCCGACAAAGCTGTGGAGACAACCCGCGAGAAACATCCCGAGTTGACAGC 236
Db      126  GCTACTACCTGATGAATAATTGGCCAAGTGTCAGAGCGGCAATATACCTCTTAAAGTA 185
QY      237  CAACGAGAGTTCCTTATCGCCAGCTCATCTGTGTACGAGACGGGTACGAGGAGCTTC 296
Db      186  CAATCAGTTGGCCGTTATATACAAGTTAAATTGGTACGAGATGGCTATGAGCAGCCATC 245
QY      297  TGATGAAGATTGAAGAGGATTACGACAGCTGCGCAGCGGACGATGAACACGAAGA 356
Db      246  TGAAGAGATCTCAGGCGTATAATGAGT-----CAACCGATGAGAACGAGACCA 296
QY      357  GTCTGACACTCCCTTCGCGCAGATCAAGAGACTATCTCTACGTTCCAACTTATCGT 416
Db      297  AACGAGCGTCAGCTTCGGCATATAACCGAGATAACCACTACACGGTCCAGTTGATTGT 356

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QY      417  GGAGTTCGGAAAGGATTCGCCAGGTTGCCAAGATTCGCAGCGCTGATCAATTAACGCT 476
Db      357  TGAAGTTTCTAAAGTCTACAGCGTTTACAAGATATACCCAGGAGACCGATCACGTT 416
QY      477  GCTTAAGGCTTCTCTCAAGTGAAGTAATGATGCTCCGAGTTCGCGCGCAGCATATGATCGCGC 536
Db      417  ACTAAAGGCTCTCTCGTCGGAGGTGATGATGCTGCGTATGCGACGCGTATGCCACAG 476
QY      537  CTCAGACAGTGTTCGTTTCGCGAACAACAACGCGTACACTCCGCGACAATACCGCAAGGC 596
Db      477  CTCGGACTCAATATCTCTCGCAATAATAGATCATATAGCGGGATTCCTTACAAAATGCG 536
QY      597  TGCATGGCTACGTCATCGAGGATCTACTGCACTTCT 634
Db      537  CGAATGGCTGATACATTTGAAGACCTGCTGCACTTCT 574

RESULT 6
CNS016YX
LOCUS   CNS016YX
DEFINITION
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN17G18 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL107379
VERSION
AL107379.1 GI:5627062
KEYWORDS
Drosophila melanogaster (fruit fly)
SOURCE
Drosophila melanogaster
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1050)
REFERENCE
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.
FEATURES
source
1..1050
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN17G18"
/clone_lib="DrosBAC"
/plasmid="pBelOBAC11"
/notes="end : SP6"

ORIGIN
Query Match 13.9%; Score 146.2; DB 10; Length 1050;
Best Local Similarity 51.6%; Pred. No. 1.1e-28;
Matches 249; Conservative 1; Mismatches 230; Indels 3; Gaps 2;

QY      478  CTTAAGGCTTGCTCAAGTGAAGTAATGATGCTCCGAGTTCGCGCGCAGATACGATCGGCC 537
Db      384  CGTTAGCGCTTGCTCGTCGGAGGTGNTGTCGTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 443
QY      538  TCAGACAGTGTTCCTGTTTCGCGAACAACAAGCGTACACTCCGCGACAACATACCGCAAGGCT 597
Db      444  TCGACTCCTNTTCTTCGCGNTNTAGTCTNTNTTCGCGGNTTCTTNCANATGGCC 503
QY      598  GGCATGGCTTACGTCATCGAGGATCTACTGCACTTCTGCGGCGTGATGATCTCTATGGCG 657
Db      504  GGAATGGCTGNTAACATTGNAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 563
QY      658  TTGACACAACATCCATTACGCGCTGCTCAGCGCTGTGTCATCTTTTTCGACCGCCAGGG 717

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QY	367	CCCTTCGCGCAGATCACAGAGATGACTATCTCTCAGCGTCCAACTTATCGTGAGTTCGCG	426
Db	96	CGCTTTGCCCACTTCAGGAGCTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCT	155
QY	427	AAGGATTCAGGTTTCGCCAAGATCTCCAGCTGATCAAAATAGCTTAAAGCT	486
Db	156	ARGCAATGCTGCTGTTCTTCGAGCTGGCGCGGAGACAGATCGCCCTCTGAAAGCA	215
QY	487	TGCTCAAGTCAGGTAAATGATGCTCCGAGTCCGCGACGATACATGCGGCTCAGACAGT	546
Db	216	TCCACTATCGAGATCATCTGCTTAGAGACAGCCAGGCGCTACAAACAGAGACAGATGT	275
QY	547	GTCTCTTCGCGAACAACCAAGCGTACATTCGCGACAATACCGCAAGCGCTGGCAT	603
Db	276	ATCACCTTCTTGAAGGACTTCACCTACAGCAAGAGACATTCACCGTGCAGCGCTGCAG	335
QY	604	GCCTACGTCATCGAGGATCTACTGCACTTCTGCGGCTGATGTACTTATGGGCTGGAC	663
Db	336	GTGGAGTTCATCAACCCCATCTTCGAGTTCGCGGCGCATGCGGCGGCTGGGCTGGAC	395
QY	664	AACATCATTTACGGCTGCTCAGCGCTGTGTCTATCTTTT---CTGACCGCGCAGGTTG	720
Db	396	GACGTGATGATCGCTTCTATCGCCATCAACATCTTCGCGCGACCGGCCCAAGTG	455
QY	721	GAGCAGCGCAATCTGTGGAGAAATCCAGCGGTACTACCTGAATAGCTCCGCTCAT	780
Db	456	CAGAGCGCGCGCGTGGAGGCGTTGACAGCGCTTACGTGGAGGCGCTGCTGCTCTAC	515
QY	781	ATCTGAACAGCTGAGCGGCTGGCGGCTGCTCGCTGATATATACGCAAGATCTCTCA	840
Db	516	ACGCGCATCAAGAGCGCGCAGACACAGC-----TGCGCTTCGCGCATGCTCATG	566
QY	841	ATCTCTCTGAGCTACGACGCTCGGATGCAAACTCCAACTGTGCTATCTCCCTCAAG	900
Db	567	AAGCTGTGAGCTTGGCAGCGCTGAGTCTGTGCACTCGGAGCGGTCTTGGCTTGGG	626
QY	901	CTCAAGAACAGAACTGCCGCTTTCTCTGAGGAGATCTGGGATGTGGCGGACATGCG	960
Db	627	CTCAGGACAAAGAGCTGCCGCTCTGCTGTGGAGATCTGGGAGCTCCAGAGTGAAG	686
QY	961	CACACCCAAACCGCGCTTA 979	
Db	687	GGCTGGCCACCCAGCCCA 705	
<p>RESULT 9  BO058428  LOCUS  DEFINITION  AGENCOURT_6794704 NIH_MGC_99 Homo sapiens cdna clone IMAGE:5814274  5', mRNA sequence.  BO058428  BO058428  BO058428.1 GI:19817768  EST.  KEYWORDS  SOURCE  ORGANISM</p>			
<p>Hominidae; Homo.  1 (bases 1 to 1031)  NIH-MGC http://mgi.nci.nih.gov/.  National Institutes of Health, Mammalian Gene Collection (MGC)  Unpublished (1999)  Contact: Robert Strausberg, Ph.D.  Email: cgaabs@mail.nih.gov  Tissue Procurement: Lou Staudt  cDNA Library Preparation: Rubin Laboratory  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  DNA Sequencing by: Agencourt Bioscience Corporation  Clone distribution: MGC clone distribution information can be  found through the I.M.A.G.E. Consortium/LLNL at:  http://image.llnl.gov  Plate: LLCM2067 row: k column: 11  High quality sequence stop: 634.  FEATURES  Location/Qualifiers  1..1031  /organism="Homo sapiens"  /mol_type="mRNA"  /db_xref="taxon:9606"  /clone="IMAGE:5814274"  /tissue_type="lymphoma, cell line"  /lab_host="DH10B (phage-resistant)"  /clone_lib="NIH_MGC_99"  /notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:  EcoRI; cDNA made by oligo-dT priming. Directionally cloned  into EcoRI/XhoI sites using the following 5' adaptor:  GGCAGCAG(G). Size-selected &gt;500bp for average insert size  1.8kb. Library constructed by Ling Hong in the laboratory  of Gerald M. Rubin (University of California, Berkeley)  using ZAP-cDNA synthesis kit (Stratagene) and Superscript  II RT (Life Technologies). Note: this is a NIH_MGC  Library."</p>			
<p>Query Match 12.0%; Score 127; DB 3; Length 1031;  Best Local Similarity 54.9%; Pred. No. 2e-23;  Matches 322; Conservative 0; Mismatches 250; Indels 15; Gaps 3;</p>		<p>QY 367 CCCTTCGCGCAGATCACAGAGATGACTATCTCAGCGTCCAACTTATCGTGAGTTCGCG 426  Db 191 CGCTTTGCCCACTTCAGGAGCTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCT 250  QY 427 AAGGATTCAGGTTTCGCCAAGATCTCGAGCTGATCAAAATAGCTTAAAGCT 486  Db 251 AAGCAAGTGCCTGCTTCTCTGAGTTCGCGCGGAGACAGATCGCCCTCTGAAAGCA 310  QY 487 TGCTCAAGTCAGGTAAATGATGCTCCGAGTCCGCGAGATACATGCGGCTCAGACAGT 546  Db 311 TCCACTATCGAGATCATCTGCTTAGAGACAGCGCGCTTACAAACAGAGACAGATGT 370  QY 547 GTTCTCTTCGCGAACAACCAAGCGTACACTTCGCGCAAACTTACCGCAAGGCTGGCAT---G 603  Db 371 ATCACCTTCTTGAAGGACTTCACCTACAGCAAGAGACGACTTCACCGTGCAGGCGCTGCAG 430  QY 604 GCCTACGTCATCGAGGATCTACTGCACTTCTGCGGCTGATGTACTTATGGGCTGGAC 663  Db 431 GTGGAGTTCATCAACCCCATCTTCGAGTTCGCGGCGCATGCGGCGGCTGGGCTGGAC 490  QY 664 AACATCCATTTACGGCTGCTCAGCGCTGTGTCTATCTTTT---CTGACCGCGCAGGTTG 720  Db 491 GACGCTGATGATCGCCCTGCTCTCATCGCCATCAACATCTTCTCGGCGCAGCGGCCCAAGCTG 550  QY 721 GAGCAGCGCAACTGTGTGGAAGAAATCCAGCGGTACTTACTCTGAATACGCTCCGCTCAT 780  Db 551 CAGGAGCGCGCGCTGAGGCGGTTCAGCAGCGCTTACGCTGAGGCGCTGCTGCTCTAC 610  QY 781 ATCTGAACAGCTGAGCGGCTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  Db 611 ACGCGCATCAAGA-----GGCGCGAGGACAGCTGCGCTTCCGCGGCTGCTGCTGCTGCT 661  QY 841 ATCTCTCTGAGCTACGACGCTCGGATGCAAACTCCAACTGTGCTATCTCCCTCAAG 900</p>	



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Db      662  AAGTGTGTGAGCCCTGCGCACGCTGAGTCTCTGTGACCTCGGAGGAGTCTTCGCTCGCG 721
Qy      901  CTCAGAACACAGAGCTGCGCCCTTCTCTCTGAGGAGATCTGGGATGT 947
Db      722  CTCAGGACAGAGCTGCGCCCTCTGCTGTGTGAGATCTGGGAGCT 768

RESULT 10
AC0077620
LOCUS   AC0077620
DEFINITION Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730478C17 product:nuclear receptor subfamily 1, group H, member 2, full insert sequence.
ACCESSION AK0077620.1 GI:26346509
VERSION   AK0077620
KEYWORDS  HTC; CAP trapper.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1963)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koude, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saichou, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome

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Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
FEATURES
Location/Qualifiers
1. 1963
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:5730478C17"
/db_xref="taxon:10090"
/clone="5730478C17"
/tissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="8 days embryo"
288..1619
/notes="unnamed protein product; nuclear receptor subfamily 1, group H, member 2 (MGD|GI:1352463, GB|NM_009473, evidence: BLASTN, 99%, match=1939) putative"
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/db_xref="GI:26346510"
/translations="MSPPTSSLDTPVGNSSQPSQTSATPTIKKEQETDPPGSEGS
SSAYIVBEDPDRKPKGPAKMLGHELCVCGDKAGFVNVLSCEGCKGPFRRS
VHGGAGRVACSGSGTCQMDAFWRKCOLCLAKCKEAGNRECVLSSEIRKRQK
QQQQPPSPSPKPTVPMPLGADQSDRQAFHAFELAIISVQIIVDFAKVPGFLQ
QCNKRFSQPKVITIMLETARYNHECTITFLKDFTSKDDFRAGLQVFEFNP
LGEEDDIALKASTIBILETARYNHECTITFLKDFTSKDDFRAGLQVFEFNP
IFPFSAMRLGDDAYALLAIINIFPSADPNVQPSRVEALQQPVYVALLSVTRIK
RPQDLRFPMLMKLVSLRTSLSSVHSQVPAFLRLQDKLPLLSLSEIWDVHE"
ORIGIN
Query Match 11.9%; Score 125.6; DB 4; Length 1963;
Best Local Similarity 53.9%; Pred. No. 5.7e-23;
Matches 332; Conservative 0; Mismatches 269; Indels 15; Gaps 3;
Qy 367 CCTTCGCGCAGATCAGAGATGACTATCTCCGCTGCAACTTATCGTGGAGTTCGG 426
Db 1032 CGCTTTGCCCACTTCACCGGCTAGGCATCATCTCGGTCCAGGAGATTGGAGCTTTGCC 1091
Qy 427 AAGGGATTGCGAGGTTTGGCAAGATCTCGCAGCTGATCAAAATACGCTGCTTAAGGCT 486
Db 1092 AAGCGTTGCGAGGTTCTTGGAGTTGGCGCGGAGACGAGATCGCCCTCTGAGGCG 1151
Qy 487 TGCTCAAGTGAGGTAATGATGCTCCGAGTCCGCGACGATACGATCGCGCTCAGACAGT 546
Db 1152 TCCACCATTCAGATCATGTTGCTAGAAACAGCCAGCGCTACAAACACGAGACAGATGC 1211
Qy 547 GTTCTGTTCCGGAACACCAAGCGGTACATCTCGGACACATACCGCAAGGCTGGCAT---G 603
Db 1212 ATCAGCTTCTGAGGAGCTTTCACATACAGCAAGACGAGCTTCCACCGTGCAGGCTTCAG 1271
Qy 604 GCCTAGCTCATCAGGATCTACTGCACTTCTCGCGGTGCGATGCTCTATGGGCTTGGAC 663
Db 1272 GTGGAATTCATCAATCCATCTTTCGAGTTCTTCGCGGCCATCGCGGCTGGGCTGGAC 1331
Qy 664 AACATCCATTCACGCGCTGCTCAGCGCTGCTCGTCACTCTTTT---CTGACCGGCCAGGCTTG 720
Db 1332 GATGCAGAGTATGCTTGTCTTATCGCCATCAACATCTTCTCAGCCGATCGSCCTAATGTG 1391
Qy 721 GAGCAGCGCACTGTTGGAGAGAAATCCAGCGGTACTACTGTAATAGCTTCGCGATCTAT 780
Db 1392 CAGGAGCCAGCGCTGTGGAGGCGCTTCGAGCAGCCCTACGTTGAGGCGCTCTCTCTCTAC 1451

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QY 781 ATCTGAAACGAGCTGAGCGGTCGGCGGTTCTCGCTCATATACGGCAAGATCTCTCTCA 840
Db 1452 ACAGGATCAAGCGCCACAGGACCAAGC-----TCGCTTCCACGCAATGCTCATG 1502
QY 841 ATCTCTCTGAGCTAGCGAGCTCGGACGATGCAAACTCCAAATGTCATCTCCCTCAAG 900
Db 1503 AAGCTGGTGAAGCTGCGCACCTCAGCTCGTGCACTCGGAGCAGGTCTTTGATTCGGA 1562
QY 901 CTCAGAACAGAAAGCTGCGGCTTCTCTCGAGGAGATCTGGGATGTGGCGGACATGTGCG 960
Db 1563 CTCAGAACAGAAAGCTGCGGCTTCTCTCGAGGAGATCTGGGATGTGGCAGGATAGGGG 1622
QY 961 CACACCCACCGCGGC 976
Db 1623 CAGCCAAAGTGCCCC 1638

RESULT 11
CN309352
LOCUS 1700599937470 GRN_PRRHEP Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN309352
VERSION CN309352.1 GI:47325766
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 651)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Pisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
TITLE Transcription characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 651 Std Error: 0.00.
FEATURES
source
1. .651
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/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PRRHEP"
/notes="oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN
Query Match 11.9%; Score 125.4; DB 7; Length 651;
Best Local Similarity 54.7%; Pred. No. 5e-23;
Matches 321; Conservative 0; Mismatches 251; Indels 15; Gaps 3;

QY 367 CCCTTCGCCGAGATCAGAGATGACTATCTCAGCGTCCAACTATTCGTGGAGTTCGCG 426
Db 74 CGCTTTGCCCACTTACGGAGTGGCCATCATCTCAGTCAGGAGATCGTGGACTTCGCT 133
QY 427 AAGGGATTGCGGGTTGCGCAAGATCTCGAGCCTGATCAATAGCTGCTTAAGGCT 486
Db 134 AAGCAATGTGCTGGTTTCTTCGAGCTGGCGGGAGACAGATCGCCCTCTCGAAGGCA 193
QY 487 TGCTCAAGTAGGTTAATGATGCTCCGAGTGGCGGACGATACGATGGCGCTCAGACAGT 546

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Db 194 TCCATATCGAGATCATGCTGTCTAGAGACAGCCAGCGGCTCAACACGAGACAGAGTGT 253
QY 547 GTTCTGTTTCGCAACAAACAGCGTACACTCGCGCAACTACCGCAAGGCTGGCAT---G 603
Db 254 ATCACCTTCTTGAAGGACTTACCTACAGCAAGGACGACTTCCACCGTGCAGGCTGCAG 313
QY 604 GCTTACGTCATCGAGGATCTACTGCACTTCTGCGGTGATGATCTCTATGCGTGGAC 663
Db 314 GTGGAGTTTATCAACCCCATCTTCGAGTTCTCGCGGGCCATCGCGGGCTGGGCTTGA 373
QY 664 AACATCCATTACGCGTCTGCTACAGCGTGTGCTCATCTTTT---CTGACCGGCGAGGGTTG 720
Db 374 GAGCTGAGTACGCGCTGCTCATCGCCATCAACATCTTCTCGGCGGACCGGCCAACGGT 433
QY 721 GAGCAGCCGCAACTGCTGTGGAAGAAATCCAGCGGTACTACCTGAATACGCTTCGCAAT 780
Db 434 CAGGAGCCGGCGCGGTGAGGCGGTTCAGCAGAGCCCTACGTCGAGAGCGCTGCTGCTCT 493
QY 781 ATCTGTAAACAGCTGAGCGGTCGGCGGTTGCTCGGTATATAGGCAAGATCTCTCTCA 840
Db 494 ACGCGCATCAAGA-----GGCGCGAGGACCAAGCTGCGCTTCCCGCGCATGCTCATG 544
QY 841 ATCTCTCTGAGCTACGCAACGCTCGCGCATGCAAACTCCAACTGTGCAATCTCCCTCAAG 900
Db 545 AAGCTGGTGAAGCTGCGCAAGCTGAGCTCTGTGCACTCGAGCAGGTCTTCGCTTGGCG 604
QY 901 CTCAGAACAGAAAGCTGCGGCTTCTTCGAGGAGATCTGGGATGT 947
Db 605 CTCAGAACAGAAAGCTGCGGCTCTGCTGTGCGAGATCTGGGAGCT 651

RESULT 12
CD673041
LOCUS 667 bp mRNA linear EST 24-JUN-2003
DEFINITION fg19g05.y1 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone
fg19g05.5', mRNA sequence.
ACCESSION CD673041
VERSION CD673041.1 GI:32174772
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 667)
AUTHORS Wistow, G., Bernstein, S.L., Ray, S., Wyatt, M.K., Behal, A.,
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
TITLE Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium
JOURNAL Mol. Vis. 8 (4), 185-195 (2002)
PUBMED 12107412
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 19 row: g column: 05
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1. .667
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="fg19g05"
/tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMDH10B"
/notes="Organ: Eye; Vector: pCMVSPORT6; A human iris
library (bx) was normalized by self-subtraction. One

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portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."

## ORIGIN

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Query Match      11.9%; Score 125.4; DB 6; Length 667;
Best Local Similarity 54.7%; Pred. No. 5e-23;
Matches 321; Conservative 0; Mismatches 251; Indels 15; Gaps 3;

QY 367 CCCTTCGCCGACATCAGAGATGACTATCTCAGGTCCCACTTATCGTGGATTGCG 426
D 10 CGCTTTGCCCACTTCCAGGAGTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCT 69
QY 427 AAGGATTTGCCAGGTTTCCGCAAGATCTCGCAGCTGTATCAAAATTACGCTGCTTAAGGCT 486
D 70 AAGCAAGTGCCTGTTTCTCGACCTGGCGCGGAGGACGATCGCCCTCTCGAAGCA 129
QY 487 TGCTCAAGTAGGTTAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCCAGACGT 546
D 130 TCCACTATCGAGATCATGCTGTAGAGACAGCCAGGCGCTACACACGACGACAGATGT 189
QY 547 GTTCTGTTCCGGAACAACCGTACACTTCGCGACAACCTACCGCAAGGCTGGCAT---G 603
D 190 ATCACTTCTTGAAGGACTTCACCTACAGCAAGGACGACTTCCACCGTCGAGGCTGCAG 249
QY 604 GCCTACCTCATCGAGGATCTACTGCATCTTCCGCGGTGCGATGACTATATGGCTTGGAC 663
D 250 GTGGAGTTTCATCAACCCCACTTCGAGTTCCTCGGCGCCATCGCGGCTGGGCTGGAC 309
QY 664 AACATCAATTACGCGCTGCTCAGCGCTGTGTCTATCTTTT---CTGACCGGCCAGGTTG 720
D 310 GACGCTGAGTAGCGCTGCTCATCGCCATCAACATCTTCTCGGCGACCGGCCCAAGTG 369
QY 721 GAGCAGCGCAACTGTGTGAAGAAATCCAGCGTACTACTGTAATACGCTCCGCAATCTAT 780
D 370 CAGGAGCGGCGCGCTGGAGCGCTTGCAGCAGCCCTACGCTGGAGGCGCTGCTGCTCTAC 429
QY 781 ATCTGTAACAGCTGAGCGGCTCGCGCGTTCGTCCTCATATACGCAAGATCTCTCA 840
D 430 ACGCGCATCAAGA-----GGCCCGAGGACGAGCTGGCGCTTCCCGCGATGCTCATG 480
QY 841 ATCTCTCTGAGCTACGACGCTCGGCATGCAAACTCCAACTGTGCTATCTCCCTCAAG 900
D 481 AAGCTGTGAGCTTGGCGACGCTGAGCTCTGTGACCTCGGAGCAGGTCTTCGCTTGGCG 540
QY 901 CTCAAGAACAGAAAGCTGCGCCCTTTCTCGAGGAGATCTGGGATGT 947
D 541 CTCAGGACAAAGAGCTGCGCCCTCTGCTGTGCGAGATCTGGGACGT 587

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## RESULT 13

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BQ214241
LOCUS      BQ214241
DEFINITION AGENCOURT 7588981 NIH_MGC_68 Homo sapiens cdna clone IMAGE:6070455
5', mRNA sequence.
ACCESSION BQ214241
VERSION   BQ214241.1 GI:20395641
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE  1 (bases 1 to 918)

```

NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabsa@mail.nih.gov](mailto:cgabsa@mail.nih.gov)  
Tissue Procurement: DCTD/DPG/Gazdar  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LLM13354 row: m column: 16  
High quality sequence stop: 626.  
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1. 918  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:6070455"  
/tissue\_type="large cell carcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_68"  
/notes="Organ: lung; Vector: pCMV-SPORT6; Site: 1: NotI;  
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.8 kb. Library constructed by Life  
Technologies."

## FEATURES

## source

## ORIGIN

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Query Match      11.9%; Score 125.4; DB 3; Length 918;
Best Local Similarity 54.7%; Pred. No. 5.4e-23;
Matches 321; Conservative 0; Mismatches 251; Indels 15; Gaps 3;

QY 367 CCCTTCGCCGACATCAGAGATGACTATCTCAGGTCCCACTTATCGTGGATTGCG 426
D 32 CGCTTTGCCCACTTCCAGGAGTGGCCATCATCTCAGTCCAGGATCTGGGACTTCGCT 91
QY 427 AAGGATTTGCCAGGTTTCCGCAAGATCTCGCAGCTGTATCAAAATTACGCTGCTTAAGGCT 486
D 92 AAGCAAGTGCCTGTTTCTCGAGCTGGCGCGGAGGACCAGATCGCCCTCTGAGGCA 151
QY 487 TGCTCAAGTAGGTAATGATGCTCCGAGTCCGCGACGATACGATGGCGCTCAGACGT 546
D 152 TCCACTATCGAGATCATGCTGTAGAGACAGCAGCGCGCTACCAACGACGACAGATGT 211
QY 547 GTTCTGTTCCGAAACAACAGCGTACCTCGCGACAACCTACCGAAGCTGGCAT---G 603
D 212 ATCACTTCTTGAAGGACTTCACTACGACGACGACTTCCACCGTGAGGCTGCTGCTCAG 271
QY 604 GCCTACGCTACGAGGATCTACTGCACTTTCGCGGTGCAATGTACTCTATGGGTTGGAC 663
D 272 GTGGAGTTTCATCAACCCCACTTTCGAGTTCTCGCGGCCATCGCGGCTGGGCTGGAC 331
QY 664 AACATCAATTACGCGTGTCTCAGGCTGTGCTCATCTTTT---CTGACCGGCCAGGTTG 720
D 332 GACGCTGAGTACGCGCTGCTCATCGGCATCAACATCTTCTCGGCCGACCGGCCCAAGTG 391
QY 721 GAGCAGCGCAACTGTGTGAAGAAATCCAGCGTACTTACCTGAATACGCTCCGCTCAT 780
D 392 CAGGAGCGGCGCGGTGGAGGCTTTCAGACGCCCTACGAGGCGCTGCTGCTGCTCTAC 451
QY 781 ATCTTGAAACAGCTGAGCGGCTCGCGCGTTCGTCGCTCATATACGCAAGATCTCTCA 840
D 452 ACGGCATCAAGA-----GGCCCGAGGACGAGCTGGCTTCCGCGCATGCTCATG 502
QY 841 ATCTCTCTGAGTACGCGCTCGGATGCAAACTCCAACTGTGCTATCTCCCTCAAG 900
D 503 AAGCTGTGAGCTTGGCGACGCTGAGCTCTGTGCACTCGGAGCAGGTCTTCGCTTGGCG 562
QY 901 CTCAAGAACAGAAAGCTGCGCCCTTTCTCGAGGAGATCTGGGATGT 947
D 563 CTCAGGACAAAGAGCTGCGCGCTCTGCTGTGCGAGATCTGGGACGT 609

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RESULT 14
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LOCUS
DEFINITION Homo sapiens NR1H2 gene, VIRTUAL TRANSCRIPT, partial sequence,
DQ052757 genomic survey sequence.
DQ052757
ACCESSION DQ052757.1 GI:66898704
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (ar) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
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/chromosome="19"
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/genes="NR1H2"
/locus_tag="HC13297"
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Query Match 11.9%; Score 125.4; DB 11; Length 1386;
Best Local Similarity 54.7%; Pred. No. 6e-23;
Matches 321; Conservative 0; Mismatches 251; Indels 15; Gaps 3;
QY 367 CCCTTCGCCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAGTTGCGG 426
DB 799 CGCTTTCGCCACTTCACGAGCTGGCCATCATCTCAGTCAGGAGATCGTGGACTTCGCT 858
QY 427 AAGGATGTCAGGGTTGGCGAGATCTCGAGCTGATCAAAATACGCTGCTTAAAGGCT 486
DB 859 AAGCAAGTGGCTGGTTTCTCTGAGCTGGCGCGGAGGACAGATCGCCCTCTGAGGCA 918
QY 487 TGCTCAAGTGGGTAAATGATGCTCCGAGTCCGCGAGCAGATACGATGCGGCTCAGACGT 546
DB 919 TCCACTATCAGATCATGCTGCTAGAGACAGCCAGCGCGCTACCAACCCAGACAGAGTGT 978
QY 547 GTTCTGTTCCGGAACCAACAGCGGTACACTCGCGACAACTACCGAAGGCTGGCAT---G 603
DB 979 ATCACTTCTTGAAGGACTTCACCTACAGCAGAGACGACTTCACCGTGAGGCTGCAG 1038
QY 604 GCCTACGTCATCGAGGATCTACTGCACTTTCGCGGTCGATGTACTCTATGGCGTTGGAC 663
DB 1039 GTGAGTTTATCAACCCCACTTTCAGTTCCTCGCGGCCATCGCGCGGCTGGGCTGGAC 1098
QY 664 AACATCATTAAGCGCTGCTCAGGCTGTGTCATCTTTT---CTGACCGCGCAGGTTG 720
DB 1099 GACGCTGAGTACGCGCTGCTCATCGCCATCAACATCTTTCGCGCGGACCGGCCCAACGTG 1158
QY 721 GAGCAGCGCACTGTGTGGAGAAATCCAGCGGTACTACCTGTAATAGCTCCGCACTAT 780

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Db 1159 CAGGAGCCGGCCGGCTGGAGGGCTTTGAGCAGAGCCCTAGCTGGAGGCGCTGCTCTCTAC 1218
QY 781 ATCTTGAAACCACTGAGCGGGTTCGGCGGCTTCGTCGTCATATACGGAAGATCTCTCA 840
Db 1219 AGCGCATCAAGA-----GGCGCAGGACCACTGCGCTTCGCGGCAATGCTCATG 1269
QY 841 ATCTCTCTGAGCTAGCAGCGCTCGGCACTGCAAACTCCAACTGCAATGCTCTCCCTCAAG 900
Db 1270 AAGCTGCTGAGCTCGGCACTGAGCTCTGTGCACTCGGACAGGCTTCGCGCTTGGCG 1329
QY 901 CTCAGAAACAGAAAGCTCGCGCTTTCTCTCGAGGAGATCTGGGATGT 947
Db 1330 CTCAGGACAAGAGCTCGCGCTCTCTGCTCGGAGATCTGGGAGCT 1376

RESULT 15
LOCUS
DEFINITION CR614375 1685 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DM011YB14 of Fetal liver of Homo sapiens
(human).
ACCESSION CR614375
VERSION CR614375.1 GI:50495182
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1685)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
REFERENCE 2 (bases 1 to 1685)
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and ScaI V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1685
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/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 11.9%; Score 125.4; DB 4; Length 1685;
Best Local Similarity 54.7%; Pred. No. 6.2e-23;
Matches 321; Conservative 0; Mismatches 251; Indels 15; Gaps 3;
QY 367 CCCTTCGCCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAGTTGCGG 426
Db 731 CGCTTTCGCCACTTCACGAGCTGGCCATCATCTCAGTCAGGAGATCGTGGACTTCGCT 790
QY 427 AAGGATGTCAGGGTTTCGCCAAGATCTCGCGACCTGATCAAAATACGCTGCTTAAAGGCT 486
Db 791 AAGCAAGTGGCTGGTTTCTCTGAGCTGGCGCGGAGGACAGATCGCCCTCTGAGGCA 850
QY 487 TGCTCAAGTGGGTAAATGATGCTTCGAGTTCGCGCGCAGATACGATGCGGCTCAGACGT 546
Db 851 TCCACTATCAGATCATGCTGCTAGAGACAGCGCGCTACCAACCCAGACAGAGTGT 910
QY 547 GTTCTGTTCCGGAACCAACAGCGGTACACTCGCGACAACTACCGCAAGGCTGGCAT---G 603

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Db	911	ATCACCTTCTTGAAGGACTTCACTACAGCAAGACGACTTCCACCGTCAGGCGCTGCAG	970
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Db	971	GTGGAGTTTCATCAACCCCATCTTCGAGTTCTCGGGGCCATCGGGCGCTTGGGCCCTGGAC	1030
Qy	664	AACATCCATTAACGCGCTGTCTCAGCGCTGTCTGTCATCTTTT---CTGACCGCCGACGGTTG	720
Db	1031	GACGCTGAGTACGCCCTTGCTCATCGCCATCAACATCTTCTCGGCGGACCGGCCCAACGCTG	1090
Qy	721	GAGCAGCCGCNACTGTGTGGAAGAAATCCAGCGGTACTACCTGAATACGCTCCGCATCTAT	780
Db	1091	CAGGAGCCGGCGCGTGGAGGGCTTGCAGCAGCCCTACGTGGAGGCGCTGCTGCTCTAC	1150
Qy	781	ATCCTGAACAGCTGAGCGGGTCGCGCGTTGTCGTGCTCATATACGGCAAGATCCTCTCA	840
Db	1151	ACGGCATCAAGA-----GGCCGACGAGCCAGCTGCGCTTCCCGCGCATGCTCATG	1201
Qy	841	ATCCTCTCTGAGCTACGACGCTCGGATCGAAAACTCCAAATATGTGTCATCTCCCTCAAG	900
Db	1202	AAGCTGTGTAGCCTTCGCACGCTGAGCTCTGTGCACTCGAGCAGGTCCTTCGCTTCGCG	1261
Qy	901	CTCAAGACAGAAAGCTGCCGCTTTCTCGAGGAGATCTGGATGT	947
Db	1262	CTCAGACAGAAAGCTGCCGCTCTGCTCTCGAGATCTGGAGCT	1308

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2006, 01:12:44 ; Search time 661 Seconds  
(without alignments)

10627.210 Million cell updates/sec

Title: US-09-965-703A-3

Perfect score: 1054

Sequence: 1 cctgagtgcgtagtagccga.....gtccggcgcgcgtgctctga 1054

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1054	100.0	1054	6 AAS68150	AbS68150 DNA encod
3	1054	100.0	1054	6 Abt08306	Abt08306 Ecr-based
4	1054	100.0	1054	6 AAL4974	Aal4974 C fumifer
5	1054	100.0	1054	6 AAS70112	AbS70112 Spruce bu
6	1054	100.0	1054	13 ADR42608	Adr42608 Choriston
7	1054	100.0	1054	13 ADR57970	Adr57970 Choriston
8	1054	100.0	1054	13 ADR90401	Adr90401 DNA of Sp
9	1054	100.0	1288	4 AAS15631	Aas15631 Spruce bu
10	1054	100.0	1288	6 AAS68144	AbS68144 DNA encod
11	1054	100.0	1288	6 Abt08298	Abt08298 Ecr-based
12	1029.4	97.7	1290	6 ABK49451	AbK49451 DNA encod
13	1029.4	97.7	1290	9 ACF36056	Acf36056 C. fumife
14	1010.2	95.8	1073	6 ABK49461	AbK49461 DNA encod
15	1010.2	95.8	1073	9 ACF36064	Acf36064 C. fumife
16	1010.2	95.8	1073	12 ADH01013	Adh01013 Spruce bu
17	1010.2	95.8	1073	12 ADH08096	Adh08096 Spruce bu
18	1005	95.4	1110	4 AAS15632	Aas15632 Spruce bu
19	1005	95.4	1110	6 Abt08308	Abt08308 Ecr-based

20	1005	95.4	1542	4 AAS15656	Aas15656 Spruce bu
21	1005	95.4	1542	6 Abt08307	Abt08307 Ecr-based
22	1002	95.1	1623	6 AAS70117	AbS70117 Spruce bu
23	960	91.1	960	4 AAS15635	Aas15635 Spruce bu
24	960	91.1	960	6 AAS68117	AbS68117 DNA encod
25	960	91.1	960	6 Abt08278	Abt08278 Ecr-based
26	929	88.1	1247	4 AAS15666	Aas15666 Spruce bu
27	735	69.7	735	4 AAS15634	Aas15634 Spruce bu
28	735	69.7	735	6 AAS68115	AbS68115 DNA encod
29	735	69.7	735	6 Abt08276	Abt08276 Ecr-based
30	636.4	60.4	2126	3 AAL10312	AaA10312 European s
31	623.4	59.1	2840	6 Abt07274	Abt07274 Manduca s
32	623.4	59.1	2840	10 ADF49073	Adf49073 Manduca s
33	623.4	59.1	2840	12 ADI33132	Adi33132 Tobacco h
34	621.6	59.0	1500	6 Abt07331	Abt07331 ChimERIC
35	621.6	59.0	1500	10 ADF49139	Adf49139 Ecdysone
36	621.6	59.0	1767	6 Abt07367	Abt07367 ChimERIC
37	621.6	59.0	1767	10 ADF49192	Adf49192 Ecdysone
38	617.4	58.6	1863	6 Abt07377	Abt07377 ChimERIC
39	617.4	58.6	1863	10 ADF49208	Adf49208 Ecdysone
40	617.2	58.6	1848	6 Abt07376	Abt07376 ChimERIC
41	617.2	58.6	1848	10 ADF49206	Adf49206 Ecdysone
42	617	58.5	1518	6 Abt07344	Abt07344 ChimERIC
43	617	58.5	1518	10 ADF49165	Adf49165 Ecdysone
44	617	58.5	3972	6 Abt07353	Abt07353 Ecdysone
45	617	58.5	3972	10 ADF49176	Adf49176 Ecdysone

## ALIGNMENTS

RESULT 1

AAS15633

ID AAS15633 standard; DNA; 1054 BP.

XX

AC AAS15633;

XX

29-JAN-2002 (first entry)

XX

DE Spruce budworm Ecdysone receptor ligand binding domain CfEcrDEF DNA.

XX

KW Spruce budworm; Ecdysone receptor; Ecr; ligand binding domain; ds;

KW retinoid X receptor; RXR; DNA-binding domain; transactivation domain;

KW nuclear receptor; ultraspiracle; gene therapy; protein production;

KW antibody production; high throughput screening; HTS; transgenic plant;

KW transgenic animal; CfEcrDEF.

XX

OS Choristoneura fumiferana.

XX

FH Key

CDS

FT

FT

FT

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FT

FT

FT

FT

Location/Qualifiers

1. .1005

/tag= a

/product= "Ecr ligand binding domain"

/partial

/note= "No start codon"

WO200170816-A2.

27-SEP-2001.

21-MAR-2001; 2001WO-US009050.

22-MAR-2000; 2000US-0191355P.

20-FEB-2001; 2001US-0269799P.

(ROHM ) ROHM & HAAS CO.

Palli SR, Kapitskaya MZ, Cress DE;

WPI; 2001-656841/75.

P-PSDB; AAU10257.

Ecdysone and retinoid X receptor based inducible gene expression systems

PT for use in e.g. gene therapy, large scale production of proteins and cell  
 PT -based high-throughput screening assays.

PS Claim 7; Page 90; 144pp; English.

XX The invention relates to Ecdysone and retinoid X receptor based inducible  
 CC gene expression systems useful for modulating gene expression in host  
 CC cells. The gene expression system encodes a polypeptide with a DNA-  
 CC binding domain recognizes a response element associated with a gene whose  
 CC expression is to be modulated and/or a ligand binding domain (LBD)  
 CC comprising a LBD from a nuclear receptor and a second gene expression  
 CC cassette capable of being expressed in a host cell comprising a  
 CC polynucleotide sequence encoding a second polypeptide comprising a trans-  
 CC activation domain and/or a LBD comprising a LBD from a nuclear receptor  
 CC other than ultraspiracle (USP) the trans-activation domain is from a  
 CC nuclear receptor other than an ecdysone receptor, a retinoid X receptor  
 CC or a USP receptor and the LBDs from the first and second polypeptides are  
 CC different and dimerize). The ecdysone and retinoid X receptor based  
 CC inducible gene expression systems useful for modulating gene expression  
 CC in host cells, for use in gene therapy, large scale production of  
 CC proteins and antibodies, cell-based high-throughput screening assays  
 CC (HTS), functional genomic and regulation of traits in transgenic plants  
 CC and animals. The present sequence encodes a Spruce budworm Ecdysone  
 CC receptor ligand binding domain for use in an inducible gene expression  
 CC system of the invention

XX Sequence 1054 BP; 258 A; 318 C; 273 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 1054; DB 4; Length 1054;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-281;  
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGAGTGGCTAGTACCGGAGCTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60  
 DB 1 CCTGAGTGGCTAGTACCGGAGCTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60  
 QY 61 AAGGAGAGACAACTGCTGTGACGACGAGCGGTGACGACCAATGCCGCCATT 120  
 DB 61 AAGGAGAGACAACTGCTGTGACGACGAGCGGTGACGACCAATGCCGCCATT 120  
 QY 121 ATGCAAGTGTGAACCTCCACCTCTGGAAGCAGCAGGATTCACGAAGTGGTCCCAAGGTTT 180  
 DB 121 ATGCAAGTGTGAACCTCCACCTCTGGAAGCAGCAGGATTCACGAAGTGGTCCCAAGGTTT 180  
 QY 181 CTCTCCGACAACTGTTGGAGACAAACCGGAGAAAATATCCCTCGATGGACAGCCAAAC 240  
 DB 181 CTCTCCGACAACTGTTGGAGACAAACCGGAGAAAATATCCCTCGATGGACAGCCAAAC 240  
 QY 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGACGAGCGGTACGAGCAGCCTTCTGAT 300  
 DB 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGACGAGCGGTACGAGCAGCCTTCTGAT 300  
 QY 301 GAAGATTGGAAGAGGATTACGACAGCTGGCAGCAACGCGACGATGAAGAAACGAAGAGTCT 360  
 DB 301 GAAGATTGGAAGAGGATTACGACAGCTGGCAGCAACGCGACGATGAAGAAACGAAGAGTCT 360  
 QY 361 GACACTCCCTTCGCGAGATCAGAGATGACTATCTCAGGTCGAGTACGATGCGGCTCTCA 420  
 DB 361 GACACTCCCTTCGCGAGATCAGAGATGACTATCTCAGGTCGAGTACGATGCGGCTCTCA 420  
 QY 421 TTGCGAAGGGATTGCGCAGGGTTCGCAAGATCTCGCAGGCTGATCAAAATACGCTGCTT 480  
 DB 421 TTGCGAAGGGATTGCGCAGGGTTCGCAAGATCTCGCAGGCTGATCAAAATACGCTGCTT 480  
 QY 481 AAGGCTTGCTCAAGTGAAGTAAATGATCTCCGAGTCCGCGGACGATACGATGCGGCTCA 540  
 DB 481 AAGGCTTGCTCAAGTGAAGTAAATGATCTCCGAGTCCGCGGACGATACGATGCGGCTCA 540  
 QY 541 GACAGTGTCTGTTCCGCGAACAACCAAGCGGTACACTCGCGACAACTACCGCAAGGCTGGC 600  
 DB 541 GACAGTGTCTGTTCCGCGAACAACCAAGCGGTACACTCGCGACAACTACCGCAAGGCTGGC 600  
 QY 601 ATGSCCTACGTCATCGAGGATCTACTGCACTTCTGCGGTCGATGTACTCTATGGCGTTG 660

DB 601 ATGGCTAGCTCATCGAGGATCTACTGCACTTCTGCGGTGCAATGACTCTATGGCTTG 660  
 QY 661 GACAAATCCATTACCGGCTCTCAAGGCTGTCGTCATCTTTTCTGACCGGCCAGGTTG 720  
 DB 661 GACAAATCCATTACCGGCTCTCAAGGCTGTCGTCATCTTTTCTGACCGGCCAGGTTG 720  
 QY 721 GAGCAGCCGCAACTGGTGGAGAAATCCAGCGGTACTACTGAATACGCTCCGATCTAT 780  
 DB 721 GAGCAGCCGCAACTGGTGGAGAAATCCAGCGGTACTACTGAATACGCTCCGATCTAT 780  
 QY 781 ATCTCTGAACAGCTGAGCGGGTCCGCGCTTCTGTCGTCATATACGCGCAAGATCTCTCA 840  
 DB 781 ATCTCTGAACAGCTGAGCGGGTCCGCGCTTCTGTCGTCATATACGCGCAAGATCTCTCA 840  
 QY 841 ATCTCTCTGAGTACGCAAGCTCGGCAATGCAAAATCCAAATGTCATCTCCCTCAAG 900  
 DB 841 ATCTCTCTGAGTACGCAAGCTCGGCAATGCAAAATCCAAATGTCATCTCCCTCAAG 900  
 QY 901 CTCAGAACAGAAAGCTGCGGCTTCTTCGAGGAGATCTGGGATGTCGCGGACATGTCG 960  
 DB 901 CTCAGAACAGAAAGCTGCGGCTTCTTCGAGGAGATCTGGGATGTCGCGGACATGTCG 960  
 QY 961 CACACCAACCGCGCTATCTCTGAGTCCCGACGAATCTCTAGCCCTTGGCGCACGC 1020  
 DB 961 CACACCAACCGCGCTATCTCTGAGTCCCGACGAATCTCTAGCCCTTGGCGCACGC 1020  
 QY 1021 ATGCGCGATGCGCGCTCGCGCGCTGCTCTGA 1054  
 DB 1021 ATGCGCGATGCGCGCTCGCGCGCTGCTCTGA 1054

RESULT 2  
 ABS68150

ID ABS68150 standard; DNA; 1054 BP.

XX ABS68150;

XX 18-NOV-2002 (first entry)

XX DNA encoding ecdysone receptor ligand binding domain #6.

XX Gene expression modulation system; DNA-binding domain; ecdysone receptor;  
 XX ligand binding domain; retinoid X receptor; RXR; transactivation domain;  
 XX gene therapy; large-scale production of protein; antibody production;  
 XX functional genomic; transgenic animal; ds.

XX Choristoneura fumiferana.

XX WO200266614-A2.

XX 29-AUG-2002.

XX 20-FEB-2002; 2002WO-US005706.

XX 20-FEB-2001; 2001US-0269799P.

XX 31-MAY-2001; 2001US-0294814P.

XX 31-MAY-2001; 2001US-0294819P.

XX (ROHM ) ROHM & HAAS CO.

XX Palli SR, Kapitskaya MZ;

XX WPI; 2002-674930/72.

XX P-PSDB; ABG92570.

XX Novel ecdysone receptor/chimeric retinoid X receptor-based inducible gene  
 XX expression system useful for modulating gene expression in a host cell  
 XX for gene therapy and large-scale production of proteins and antibodies.

XX Claim 4; Page 130; 140pp; English.

XX The invention describes a gene expression modulation system (I)



comprising first and second gene expression cassettes that comprise polynucleotides encoding first and second hybrid polypeptides (P1,P2). P1 comprises a DNA-binding domain and an ecdysone receptor ligand binding domain or DNA-binding domain and a chimeric retinoid X receptor (RXR) ligand binding domain. P2 comprises a transactivation domain and RXR ligand binding domain or transactivation domain and ecdysone receptor ligand binding domain. (1) is useful for modulating the expression of a gene in a host cell, for applications such as gene therapy, large-scale production of proteins and antibodies, cell-based high throughput screening assays, functional genomics and regulation of traits in transgenic organisms. This sequence encodes an ecdysone receptor ligand binding domain useful in the creation of the gene expression modulation system

Query Match 100.0%; Score 1054; DB 6; Length 1054;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-281;  
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAGTGGTACCGAGACTCAGTGGCCCATGAGCGGAAAGAGAAAGCAAG 60  
 Db 1 CCTGAGTGGTACCGAGACTCAGTGGCCCATGAGCGGAAAGAGAAAGCAAG 60  
 Qy 61 AAGGAGAGGACAACTGCTGTGACGACGAGCGGTGGACGACCATGCGCCCATTT 120  
 Db 61 AAGGAGAGGACAACTGCTGTGACGACGAGCGGTGGACGACCATGCGCCCATTT 120  
 Qy 121 ATGCAAGTGTGAACCTCCACCTCTGAGCAGCAAGGATTCACGAGTGGTCCCAAGGTTT 180  
 Db 121 ATGCAAGTGTGAACCTCCACCTCTGAGCAGCAAGGATTCACGAGTGGTCCCAAGGTTT 180  
 Qy 181 CTCTCCGACAGCTGTTGGAGACAAACCGGCGAGAAACATCCCCAGTTGACAGCCAAAC 240  
 Db 181 CTCTCCGACAGCTGTTGGAGACAAACCGGCGAGAAACATCCCCAGTTGACAGCCAAAC 240  
 Qy 241 CAGCAGTTCCTTATGCGCAGGCTCATCTGGTACGAGCAGGTTACGAGCCTTCTGAT 300  
 Db 241 CAGCAGTTCCTTATGCGCAGGCTCATCTGGTACGAGCAGGTTACGAGCCTTCTGAT 300  
 Qy 301 GAAGATTGAAGAGATTACGACAGTGGCGAGCAAGCGGACGATGAAGAGAGAGTCT 360  
 Db 301 GAAGATTGAAGAGATTACGACAGTGGCGAGCAAGCGGACGATGAAGAGAGAGTCT 360  
 Qy 361 GACACTCCCTTCGCGCAGATCACAGAGATGACTATCTCCAGGTCCTTATCGTGGAG 420  
 Db 361 GACACTCCCTTCGCGCAGATCACAGAGATGACTATCTCCAGGTCCTTATCGTGGAG 420  
 Qy 421 TTCCGGAAGGATTGCCAGGTTGCCAGATCTCGCAGCCTGATCAAAATACGCTGCTT 480  
 Db 421 TTCCGGAAGGATTGCCAGGTTGCCAGATCTCGCAGCCTGATCAAAATACGCTGCTT 480  
 Qy 481 AAGGCTTGCTCAAGTGAAGTAAATGATCTCCGAGTCCGCGACCATACGATGCGGCTCA 540  
 Db 481 AAGGCTTGCTCAAGTGAAGTAAATGATCTCCGAGTCCGCGACCATACGATGCGGCTCA 540  
 Qy 541 GACAGTGTCTGTTGCGGACAAACCAAGCGTACACTCGCGCAACTACCGCAAGGCTGGC 600  
 Db 541 GACAGTGTCTGTTGCGGACAAACCAAGCGTACACTCGCGCAACTACCGCAAGGCTGGC 600  
 Qy 601 ATGCGCTACGTCATCGAGGATCTACTGCACTTTCGCGGTGCGATGATCTATGCGGTTG 660  
 Db 601 ATGCGCTACGTCATCGAGGATCTACTGCACTTTCGCGGTGCGATGATCTATGCGGTTG 660  
 Qy 661 GACAACTCCATTACGCGCTGCTACGCGTGTGCTGATCTTTTCTGACCGGCGAGGTTG 720  
 Db 661 GACAACTCCATTACGCGCTGCTACGCGTGTGCTGATCTTTTCTGACCGGCGAGGTTG 720  
 Qy 721 GAGCAGCGCGCAACTGTTGGAGAAATCCAGCGGTACTACTGGAATAGCTCCGATCTAT 780  
 Db 721 GAGCAGCGCGCAACTGTTGGAGAAATCCAGCGGTACTACTGGAATAGCTCCGATCTAT 780  
 Qy 781 ATCTGAAACCAAGCTGAGCGGTCGGCGGTTCTGCTGCTCATATACGGAAGATCTCTCA 840

781 ATCTGAAACAGCTGAGCGGTCGGCGGTTCTGCTGCTATATACGGAAGATCTCTCA 840  
 Qy 841 ATCTGCTCTGAGCTACGACGCTCGGCATGCAAAATCTCCAAATGTGCTATCTCCCTCAAG 900  
 Db 841 ATCTGCTCTGAGCTACGACGCTCGGCATGCAAAATCTCCAAATGTGCTATCTCCCTCAAG 900  
 Qy 901 CTCAAGAACAGAAAGCTGCGGCTTTCTCTGAGGAGATCTGGGATGTGGCGGACATGTCG 960  
 Db 901 CTCAAGAACAGAAAGCTGCGGCTTTCTCTGAGGAGATCTGGGATGTGGCGGACATGTCG 960  
 Qy 961 CACACCCCAACGCGGCTATCTCTGAGTCCCGCAGCAATCTCTAGCCCTTGGCGGACGC 1020  
 Db 961 CACACCCCAACGCGGCTATCTCTGAGTCCCGCAGCAATCTCTAGCCCTTGGCGGACGC 1020  
 Qy 1021 ATGCGCGATGCGGCTCGGCGCGCTGCTCTGA 1054  
 Db 1021 ATGCGCGATGCGGCTCGGCGCGCTGCTCTGA 1054

RESULT 3  
 ABT08306  
 ID ABT08306 standard; DNA; 1054 BP.  
 XX ABT08306;  
 AC ABT08306;  
 XX 28-NOV-2002 (first entry)  
 XX ECR-based inducible gene expression cassette related DNA SEQ ID No 53.  
 DE Gene expression modulation system; large-scale production; gene therapy;  
 KW Gene expression cassette; functional genomics; transgenic organism; ds.  
 OS Choristoneura fumiferana.  
 XX WO200266613-A2.  
 XX 29-AUG-2002.  
 XX 20-FEB-2002; 2002WO-US005235.  
 XX 20-FEB-2001; 2001US-0269799P.  
 XX 31-MAY-2001; 2001US-0294814P.  
 XX (ROHM ) ROHM & HAAS CO.  
 XX Palli SR, Kapitskaya MZ;  
 XX WPI; 2002-674929/72.  
 DR Novel ecdysone receptor/invertebrate retinoid X receptor-based inducible  
 XX gene expression system useful for modulating gene expression in host cell  
 XX for gene therapy and large-scale production of proteins and antibodies.  
 XX Claim 4; Page 116-117; 123pp; English.  
 XX The invention relates to a novel gene expression modulation system  
 CC comprising first and second gene expression cassettes that comprises  
 CC polynucleotides encoding first and second hybrid polypeptides. The gene  
 CC expression modulation system is useful for modulating the expression of a  
 CC gene in a host cell comprising the gene to be modulated, for applications  
 CC such as gene therapy, large-scale production of proteins and antibodies,  
 CC cell-based high throughput screening assays, functional genomics and  
 CC regulation of traits in transgenic organisms. This polynucleotide  
 CC sequence represents DNA relating to the gene expression cassettes of the  
 CC invention  
 XX Sequence 1054 BP; 258 A; 318 C; 273 G; 205 T; 0 U; 0 Other;  
 SQ

Query Match 100.0%; Score 1054; DB 6; Length 1054;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-281;  
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60
DB |||
1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60
QY 61 AAGGAGAGGACAAACTGCTGTGACGACGACGAGTGGACCAATGCCGCCATT 120
DB |||
61 AAGGAGAGGACAAACTGCTGTGACGACGACGAGTGGACCAATGCCGCCATT 120
QY 121 ATGCAAGTGAACCTCCACCTCTGAAGCAGCAAGGATTCACGAAGTGGTCCCAAGTTT 180
DB |||
121 ATGCAAGTGAACCTCCACCTCTGAAGCAGCAAGGATTCACGAAGTGGTCCCAAGTTT 180
QY 181 CTCTCCGACAAAGCTGTGGAGACAAACCGGACGAAACATCCCCAGTTGACAGCCAAC 240
DB |||
181 CTCTCCGACAAAGCTGTGGAGACAAACCGGACGAAACATCCCCAGTTGACAGCCAAC 240
QY 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGTACGAGCGGTACGAGCAGCCTTCTGAT 300
DB |||
241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGTACGAGCGGTACGAGCAGCCTTCTGAT 300
QY 301 GAAGATTGGAAGGATTACGAGAGTGGCAGCAGGACGAGTGAAGAGAGTCT 360
DB |||
301 GAAGATTGGAAGGATTACGAGAGTGGCAGCAGGACGAGTGAAGAGAGTCT 360
QY 361 GACACTCCCTTCGCCAGATCACAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420
DB |||
361 GACACTCCCTTCGCCAGATCACAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420
QY 421 TTCGGAAGGATTGCGCAGGTTGCGCAAGATTCGCGAGCTGATCAAAATTACGCTGCTT 480
DB |||
421 TTCGGAAGGATTGCGCAGGTTGCGCAAGATTCGCGAGCTGATCAAAATTACGCTGCTT 480
QY 481 AAGCTTGTCTCAAGTAGGTAATGATGCTCGAGTGGCGGACGATGAGTAGCGGCTCA 540
DB |||
481 AAGCTTGTCTCAAGTAGGTAATGATGCTCGAGTGGCGGACGATGAGTAGCGGCTCA 540
QY 541 GACAGTGTCTGTTCCGGAACCAACCAAGCTGTACTCGGACAACTACCGCAAGGCTGGC 600
DB |||
541 GACAGTGTCTGTTCCGGAACCAACCAAGCTGTACTCGGACAACTACCGCAAGGCTGGC 600
QY 601 ATGSCCTACGCTACGAGGATCTACTGCACTTCTGCGGTCGATGATCTATGGGTTG 660
DB |||
601 ATGSCCTACGCTACGAGGATCTACTGCACTTCTGCGGTCGATGATCTATGGGTTG 660
QY 661 GACAACTATCAATACGCGCTGCTCAGCGCTGTGTCATCTTTTGTGACCGGCGAGGTTG 720
DB |||
661 GACAACTATCAATACGCGCTGCTCAGCGCTGTGTCATCTTTTGTGACCGGCGAGGTTG 720
QY 721 GAGCAGCGCAACTGTTGGGAAGAAATCCAGCGGTACTCTGATATACGCTCCGCTAT 780
DB |||
721 GAGCAGCGCAACTGTTGGGAAGAAATCCAGCGGTACTCTGATATACGCTCCGCTAT 780
QY 781 ATCTCTGAACCAAGCTAGCGGTGCGCGGTTGCTGCTCATATATACGCAAGATCTCTCA 840
DB |||
781 ATCTCTGAACCAAGCTAGCGGTGCGCGGTTGCTGCTCATATATACGCAAGATCTCTCA 840
QY 841 ATCTCTCTGAGCTACGCAAGCTCGGATGCAAAATCTCAACATGTGCTATCTCTCAAG 900
DB |||
841 ATCTCTCTGAGCTACGCAAGCTCGGATGCAAAATCTCAACATGTGCTATCTCTCAAG 900
QY 901 CTCAAGAACAGAAAGCTGCGGCTTTCTCGAGAGATCTGGGATGTGGCGGACATGTCG 960
DB |||
901 CTCAAGAACAGAAAGCTGCGGCTTTCTCGAGAGATCTGGGATGTGGCGGACATGTCG 960
QY 961 CACACCCAAACCGCGCTATCTCTGAGTCCCGCCAGAAATCTCTAGCCCTTCGCGCAGC 1020
DB |||
961 CACACCCAAACCGCGCTATCTCTGAGTCCCGCCAGAAATCTCTAGCCCTTCGCGCAGC 1020
QY 1021 ATGCGCGATGCGGCTCGGCGCGCTGCTCTGA 1054
DB |||
1021 ATGCGCGATGCGGCTCGGCGCGCTGCTCTGA 1054
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RESULT 4
AAL49744
ID AAL49744 standard; DNA; 1054 BP.
XX
AC AAL49744;
XX
DT 28-NOV-2002 (first entry)
XX
DE C fumiferana ecdysone receptor D,E,F domains coding sequence.
XX
KW Receptor; expression system; nuclear receptor; inducible gene expression;
KW gene therapy; protein production; mutant; ecdysone receptor;
KW retinoid X receptor; GAL4; LexA; VP16; B42; p65; gene; ds.
XX
OS Choristoneura fumiferana.
XX
WO200266615-A2.
XX
PD 29-AUG-2002.
XX
PF 20-FEB-2002; 2002WO-US005708.
XX
PR 20-FEB-2001; 2001US-0269799P.
PR 21-AUG-2001; 2001US-0313908P.
XX
PA (ROHM ) ROHM & HAAS CO.
XX
PI Palli SR, Kapitskaya MZ;
XX
WP1; 2002-674931/72.
XX
PT Novel nuclear receptor polypeptides with substitution mutations, useful
PT in gene expression modulation systems which are useful in gene therapy
PT applications and cell-based high throughput screening assays.
XX
PS Example 1; Page 95; 110pp; English.
XX
CC The present invention relates to a gene expression modulation system
CC containing a mutated coding sequence for a Group B nuclear receptor
CC ligand. This is useful for modulating expression of a gene in a host
CC cell, particularly in applications such as gene therapy, large scale
CC production of proteins and antibodies, cell-based high throughput
CC screening assays, functional genomics and regulation of traits in
CC transgenic organisms. The present sequence is a coding sequence described
CC in the exemplification of the invention
XX
SQ Sequence 1054 BP; 258 A; 318 C; 273 G; 205 T; 0 U; 0 Other;
```

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Query Match 100.0%; Score 1054; DB 6; Length 1054;
Best Local Similarity 100.0%; Pred. No. 1.5e-281;
Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60
DB |||
1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60
QY 61 AAGGAGAGGACAAACTGCTGTGACGACGAGTGGACCAATGCCGCCATT 120
DB |||
61 AAGGAGAGGACAAACTGCTGTGACGACGAGTGGACCAATGCCGCCATT 120
QY 121 ATGCAAGTGAACCTCCACCTCTGAAGCAGCAAGGATTCACGAAGTGGTCCCAAGTTT 180
DB |||
121 ATGCAAGTGAACCTCCACCTCTGAAGCAGCAAGGATTCACGAAGTGGTCCCAAGTTT 180
QY 181 CTCTCCGACAAAGCTGTGGAGACAAACCGGACGAAACATCCCCAGTTGACAGCCAAC 240
DB |||
181 CTCTCCGACAAAGCTGTGGAGACAAACCGGACGAAACATCCCCAGTTGACAGCCAAC 240
QY 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGTACGAGCGGTACGAGCAGCCTTCTGAT 300
DB |||
241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGTACGAGCGGTACGAGCAGCCTTCTGAT 300
QY 301 GAAGATTGGAAGGATTACGAGAGTGGCAGCAGGACGAGTGAAGAGAGTCT 360
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Db 301 GAGATTTGAAGAGATTACGACAGCTGGGAGAGCGGACGATGAAAAAGAGAGTCT 360
Qy 361 GACATCTCCCTTCCGCGACAGATCACAGAGATGACTATCTTCAAGGTCCTCAACTTATCGTGGAG 420
Db 361 GACATCTCCCTTCCGCGACAGATCACAGAGATGACTATCTTCAAGGTCCTCAACTTATCGTGGAG 420
Qy 421 TTCCGGAAGGATTCGCGAGGTTGCGCAAGATCTCGAGCTCGATCAAAATACGCTGCTT 480
Db 421 TTCCGGAAGGATTCGCGAGGTTGCGCAAGATCTCGAGCTCGATCAAAATACGCTGCTT 480
Qy 481 AAGGCTTCTCAAGTGAAGTAAATGCTCCGAGTCCGCGACGATACGATCGAGCTGCTCA 540
Db 481 AAGGCTTCTCAAGTGAAGTAAATGCTCCGAGTCCGCGACGATACGATCGAGCTGCTCA 540
Qy 541 GACAGTGTCTTCTGCGCAACCAAGCTACACTCGCGACAACTACCGCAAGGCTGGC 600
Db 541 GACAGTGTCTTCTGCGCAACCAAGCTACACTCGCGACAACTACCGCAAGGCTGGC 600
Qy 601 ATGGCTACGTCATCGAGGATCTACTGCACTTCTGCGGTCGATGACTCTTATGCGGTTG 660
Db 601 ATGGCTACGTCATCGAGGATCTACTGCACTTCTGCGGTCGATGACTCTTATGCGGTTG 660
Qy 661 GACACATCCATTAAGCGCTGCTCACGGCTGCTGCTATCTTTCTGACCGGCGAGGTTG 720
Db 661 GACACATCCATTAAGCGCTGCTCACGGCTGCTGCTATCTTTCTGACCGGCGAGGTTG 720
Qy 721 GAGCAGCGCACTGTGTGAAGAAATCCAGCGGTACTTACCTGAATACGCTCCGCTAT 780
Db 721 GAGCAGCGCACTGTGTGAAGAAATCCAGCGGTACTTACCTGAATACGCTCCGCTAT 780
Qy 781 ATCTGAAACCAAGCTGAGCGGTGCGCGGTTCTGCTCATATATACGCGCAAGATCTCTCA 840
Db 781 ATCTGAAACCAAGCTGAGCGGTGCGCGGTTCTGCTCATATATACGCGCAAGATCTCTCA 840
Qy 841 ATCTCTCTGAGCTACGCAAGCTGCGCATGCGCAAACTCCAACTGTCATCTCCCTCAAG 900
Db 841 ATCTCTCTGAGCTACGCAAGCTGCGCATGCGCAAACTCCAACTGTCATCTCCCTCAAG 900
Qy 901 CTCAAGAACCAAGCTGCGCGCTTCTCTGAGGAGATCTGGGATGTGGCGGACATGTCG 960
Db 901 CTCAAGAACCAAGCTGCGCGCTTCTCTGAGGAGATCTGGGATGTGGCGGACATGTCG 960
Qy 961 CACACCAACCGCGCTTATCTCTGAGTCCCGGATCTCTAGCCCTTGTGCGGCGAGC 1020
Db 961 CACACCAACCGCGCTTATCTCTGAGTCCCGGATCTCTAGCCCTTGTGCGGCGAGC 1020
Qy 1021 ATCCCGATGCGCGTTCGCGCGGCTGCTCTGA 1054
Db 1021 ATCCCGATGCGCGTTCGCGCGGCTGCTCTGA 1054
```

## RESULT 5

ABS70112

ID ABS70112 standard; DNA; 1054 BP.

XX AC

XX AC

XX AC

XX ABS70112;

XX 25-NOV-2002 (first entry)

XX Spruce budworm Ecr D,E and F domain sequence.

XX DE Gene expression modulation system; gene expression cassette; promoter;

XX KW transactivation domain; DNA-binding domain; response element; LBD; DBD;

XX KW Group H nuclear receptor ligand binding domain; gene therapy; TD; ECR;

XX KW ds.

XX OS Choristoneura fumiferana.

XX OS

XX XX

XX PN W0200266612-A2.

XX XX

XX XX

XX 29-AUG-2002.

XX

```
PF 20-FEB-2002; 2002WO-US0005090.
XX
PR 20-FEB-2001; 2001US-0269799P.
PR 21-AUG-2001; 2001US-0313925P.
XX
PA (ROHM ) ROHM & HAAS CO.
XX
PI Palli SR, Kumar MB, Cress DE, Fujimoto TT;
XX WPI; 2002-682765/73.
XX
PT Novel gene expression modulation system useful for modulating expression
PT of a gene of interest, comprising a Group H nuclear receptor ligand
PT binding domain comprising a substitution mutation.
XX
PS Example 1; Page 112; 148pp; English.
XX
CC The present invention relates to a new gene expression modulation system.
CC The invention comprises a gene expression cassette, capable of being
CC expressed in a host cell, comprising a polynucleotide that encodes a
CC polypeptide comprising a transactivation domain, a DNA-binding domain
CC that recognises a response element associated with a gene whose
CC expression is to be modulated, and a Group H nuclear receptor ligand
CC binding domain (LBD). The invention is useful for modulating the
CC expression of the gene in a host cell which involves introducing into the
CC host cell, and introducing into the host cell a ligand, where the gene to
CC be modulated is a component of a gene expression cassette comprising a
CC response element by the DBD (DNA-binding domain), a promoter that is
CC activated by the TD (transactivation domain) and a gene whose expression
CC is to be modulated, where upon introduction of the ligand into the host
CC cell, expression of the desired gene is modulated. The inducible gene
CC expression system and its use for modulating gene expression in a host
CC cell overcome the limitations of currently available inducible expression
CC systems and provides an effective means for controlling gene expression.
CC The present nucleic acid sequence represents a DNA sequence that was used
CC in the methods of the invention
XX
```

SQ Sequence 1054 BP; 258 A; 318 C; 273 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 1054; DB 6; Length 1054;

Best Local Similarity 100.0%; Pred. No. 1.5e-281;

Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAAAGACACAG 60
Db 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAAAGACACAG 60
Qy 61 AAGGAGAGGACAAACTGCTGTGAGCAGCAGCGGTGACACCATGCGGCCCATTT 120
Db 61 AAGGAGAGGACAAACTGCTGTGAGCAGCAGCGGTGACACCATGCGGCCCATTT 120
Qy 121 ATGCAAGTGAACCTCCACCTCTGAGCAGCAGGATTCACGAAGTGGTCCCAAGGTTT 180
Db 121 ATGCAAGTGAACCTCCACCTCTGAGCAGCAGGATTCACGAAGTGGTCCCAAGGTTT 180
Qy 181 CTCTCCGACAAAGCTGTTGGAGACAAACCCGCGAGAAAACATCCCGAGTTGACAGCCAAC 240
Db 181 CTCTCCGACAAAGCTGTTGGAGACAAACCCGCGAGAAAACATCCCGAGTTGACAGCCAAC 240
Qy 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGGTACAGGACGGGTACGAGCAGCCTTCTGAT 300
Db 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGGTACAGGACGGGTACGAGCAGCCTTCTGAT 300
Qy 301 GAGATTTGAAGAGGATTCGCGAGCGTGGCAGCAGCGGACCGACCGATGAAAACGAGAGTCT 360
Db 301 GAGATTTGAAGAGGATTCGCGAGCGTGGCAGCAGCGGACCGACCGATGAAAACGAGAGTCT 360
Qy 361 GACACTCCCTTTCGCGCAGATCAAGAGATGACTATCTCTACGGTCCAACTTATCGTGGAG 420
Db 361 GACACTCCCTTTCGCGCAGATCAAGAGATGACTATCTCTACGGTCCAACTTATCGTGGAG 420
Qy 421 TTCGGAAGGATTCGCGAGGTTGCGCAAGATCTCGAGCTCGATCAAAATACGCTGCTT 480
```

421 TTCCGGAAGGATTTCCAGGGTTCCCAAGATCTCGAGCTGATCAAAATACGCTGCTT 480  
 481 AAGCTTGTCTCAAGTGAAGTAATGATCTCCGAGTCCGCGACGATGAGTGGGCTCA 540  
 481 AAGGCTTGTCTCAAGTGAAGTAATGATCTCCGAGTCCGCGACGATGAGTGGGCTCA 540  
 541 GACAGTGTCTCTGTTCCGGAACCAACCAAGGATGACACTCGCGACAACTACCGCAAGGCTGGC 600  
 541 GACAGTGTCTCTGTTCCGGAACCAACCAAGGATGACACTCGCGACAACTACCGCAAGGCTGGC 600  
 601 ATGGCCCTACGATCGAGGATCTACTGCACTTCTGCGGCTGATGATCTATGGGCTTG 660  
 601 ATGGCCCTACGATCGAGGATCTACTGCACTTCTGCGGCTGATGATCTATGGGCTTG 660  
 661 GACAGATTCATACGGCTGCTCAAGGCTGTGTCATCTTTTCTGACCGGCCAGGGTTG 720  
 661 GACAGATTCATACGGCTGCTCAAGGCTGTGTCATCTTTTCTGACCGGCCAGGGTTG 720  
 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTGATGATGATGATGATGATGATGAT 780  
 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTGATGATGATGATGATGATGATGAT 780  
 781 ATCTGAAACAGCTGAGCGGTCGGCGCTTCTGCGTCTATATACGGCAAGATCTCTCTCA 840  
 781 ATCTGAAACAGCTGAGCGGTCGGCGCTTCTGCGTCTATATACGGCAAGATCTCTCTCA 840  
 841 ATCTCTCTGAGTACGACGCTCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGG 900  
 841 ATCTCTCTGAGTACGACGCTCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGG 900  
 901 CTCAAGAAACAGAAAGCTGCGCGCTTCTCTGAGGAGATCTGGATGCGGAGCATGTGCG 960  
 901 CTCAAGAAACAGAAAGCTGCGCGCTTCTCTGAGGAGATCTGGATGCGGAGCATGTGCG 960  
 961 CACACCCAAACCGCGCTTCTCTGAGTCCCGCAAGATCTCTAGCCCTCGCGGACGCG 1020  
 961 CACACCCAAACCGCGCTTCTCTGAGTCCCGCAAGATCTCTAGCCCTCGCGGACGCG 1020  
 1021 ATGCGCGATCGCGCTCGCGCGCTGCTCTGA 1054  
 1021 ATGCGCGATCGCGCTCGCGCGCTGCTCTGA 1054

RESULT 6  
 ADR42608  
 ID ADR42608 standard; DNA; 1054 BP.  
 AC ADR42608;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Choristoneura fumiferana ecdysone receptor (EcR).  
 XX  
 KW spruce budworm; oxadiazoline ligand; gene expression modulation;  
 KW gene expression cassette; ecdysone receptor complex; transgenic;  
 KW genetic engineering; ecdysone receptor; EcR; gene; ds.  
 XX  
 OS Choristoneura fumiferana.  
 XX  
 PN US2004171651-A1.  
 XX  
 PD 02-SEP-2004.  
 XX  
 PF 19-FEB-2004; 2004US-00783810.  
 XX  
 PR 21-FEB-2003; 2003US-0449467P.  
 XX  
 PA (HORM/) HORMANN R E.  
 PA (CHOR/) CHORTYK O.  
 PA (LEDP/) LE D P.  
 XX  
 PI Horman RE, Chortyk O, Le DP;

DR WPI; 2004-651695/63.  
 XX New oxadiazoline ligands for regulating expression of nuclear receptor-  
 PT based inducible genes in genetic engineering.  
 XX Example 2; SEQ ID NO 1; 72pp; English.  
 PS  
 XX The invention describes oxadiazoline ligands. Also described are:  
 CC modulating expression of a target gene in a host cell involving  
 CC contacting the host cell with (i), the host cell includes first and  
 CC second gene expression cassettes, or gene expression modulation system is  
 CC introduced in the host cell; regulating endogenous or heterologous gene  
 CC expression in a transgenic subject involving contacting (i) with an  
 CC ecdysone receptor complex within the cells of the subject, the cells  
 CC further contain a DNA binding sequence for the ecdysone receptor complex  
 CC when in combination with the ligand, and formation of an ecdysone  
 CC receptor complex-ligand DNA binding sequence complex induces expression  
 CC of the gene; and producing a polypeptide involving selecting a cell which  
 CC is insensitive to exposure to the ligand of formula (I), introducing into  
 CC the cell a DNA construct and an ecdysone receptor complex, and exposing  
 CC the cell to (I), the DNA construct comprises exogenous gene encoding the  
 CC polypeptide, and a response element, the ecdysone receptor complex  
 CC comprises DNA binding domain, a binding domain for the ligand, and  
 CC transactivation domain. The ligands are useful for regulating expression  
 CC of endogenous as well as heterologous genes in a transgenic subject (e.g.  
 CC plant or mammal) during genetic engineering. The ligands provide an  
 CC improved inducible gene expression system in both prokaryotic and  
 CC eukaryotic host cells. This sequence represents Choristoneura fumiferana  
 CC ecdysone receptor (EcR), used in the creation of a nuclear receptor-based  
 CC inducible gene expression system.  
 XX  
 SQ Sequence 1054 BP; 258 A; 318 C; 273 G; 205 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1054; DB 13; Length 1054;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-281;  
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGTAGTGGTGTAGTACCCGAGACTCAGTGGCGCATGAGCGGAAAGAGAAAGACAG 60  
 DB 1 CTGTAGTGGTGTAGTACCCGAGACTCAGTGGCGCATGAGCGGAAAGAGAAAGACAG 60  
 QY 61 AAGGAGAAGGACAAACTGCTGTGACGACGAGCGTGGAGACACATCGGCCCAT 120  
 DB 61 AAGGAGAAGGACAAACTGCTGTGACGACGAGCGTGGAGACACATCGGCCCAT 120  
 QY 121 ATGCACTGTGAACCTCCACCTCTCTGAAGCAGCAAGGATTCACGAAGTGTCCCAAGGTTT 180  
 DB 121 ATGCACTGTGAACCTCCACCTCTCTGAAGCAGCAAGGATTCACGAAGTGTCCCAAGGTTT 180  
 QY 181 CTCTCCGACAGCTGTGGAGACAAACCGCGCAGAAAAATATCCCGAGTTGACAGCCAAC 240  
 DB 181 CTCTCCGACAGCTGTGGAGACAAACCGCGCAGAAAAATATCCCGAGTTGACAGCCAAC 240  
 QY 241 CAGCAGTCTCTTATCCCGAGGCTCATCTGTGACCGAGCGGTGACGAGCGCTTCGTAT 300  
 DB 241 CAGCAGTCTCTTATCCCGAGGCTCATCTGTGACCGAGCGGTGACGAGCGCTTCGTAT 300  
 QY 301 GAAGATTTGAAGAGGATTAACGACAGCTGTGGCAGCAAGCGGACGATGAAACGAGAGTCT 360  
 DB 301 GAAGATTTGAAGAGGATTAACGACAGCTGTGGCAGCAAGCGGACGATGAAACGAGAGTCT 360  
 QY 361 GACATCTCCCTTCCCGCAGATCAAGAGATGATATCTCTCAAGTCAACTTATCTGTGGAG 420  
 DB 361 GACATCTCCCTTCCCGCAGATCAAGAGATGATATCTCTCAAGTCAACTTATCTGTGGAG 420  
 QY 421 TTCCGGAAGGATTTGCGCAGGTTTCCGCAAGATCTCCGAGCTGATCAAAATACGCTGCTT 480  
 DB 421 TTCCGGAAGGATTTGCGCAGGTTTCCGCAAGATCTCCGAGCTGATCAAAATACGCTGCTT 480  
 QY 481 AAGGCTTGTCTCAAGTGAAGTGAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCA 540  
 DB 481 AAGGCTTGTCTCAAGTGAAGTGAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCA 540

Qy 541 GACAGTGTCTGTTCCGGAACACCAAGCGTACACTCGCGCAAACTACCGCAAGGCTGGC 600  
Db 541 GACAGTGTCTGTTCCGGAACACCAAGCGTACACTCGCGCAAACTACCGCAAGGCTGGC 600  
Qy 601 ATGCGCTACGTCATCGAGGATCTACTGACCTTCGCGGTGCGATGCTCTATCGCGTTG 660  
Db 601 ATGCGCTACGTCATCGAGGATCTACTGACCTTCGCGGTGCGATGCTCTATCGCGTTG 660  
Qy 661 GACAACATCCATTACGCGCTGCTCACGCGTGTGCTGCTATCTTTCTGACCGGCCAGGTTG 720  
Db 661 GACAACATCCATTACGCGCTGCTCACGCGTGTGCTGCTATCTTTCTGACCGGCCAGGTTG 720  
Qy 721 GAGCAGCGCAACTGTTGGAGAAATCAGCGGTACTACCTGAATAGCTCCGCACTAT 780  
Db 721 GAGCAGCGCAACTGTTGGAGAAATCAGCGGTACTACCTGAATAGCTCCGCACTAT 780  
Qy 781 ATCTCTGAACAGCTGAGCGGTGCGCGTTCGTCGTCATATACGCGCAAGCTCTCA 840  
Db 781 ATCTCTGAACAGCTGAGCGGTGCGCGTTCGTCGTCATATACGCGCAAGCTCTCA 840  
Qy 841 ATCTCTCTGAGCTACGCAAGCTCGGCATGCGCAAACTCCAACTGTCATCTCCCTCAAG 900  
Db 841 ATCTCTCTGAGCTACGCAAGCTCGGCATGCGCAAACTCCAACTGTCATCTCCCTCAAG 900  
Qy 901 CTGAAGAACAGAAAGCTGCGGCTTTCTCGAGAGATCTGGGATGTGGCGGACATGTG 960  
Db 901 CTGAAGAACAGAAAGCTGCGGCTTTCTCGAGAGATCTGGGATGTGGCGGACATGTG 960  
Qy 961 CACACCCAAACCGCGCTATCTCGAGTCCCGGCTGCTCTGA 1054  
Db 961 CACACCCAAACCGCGCTATCTCGAGTCCCGGCTGCTCTGA 1054  
Qy 1021 ATCGCCGATGCGCGTCCGCGCGCTGCTCTGA 1054  
Db 1021 ATCGCCGATGCGCGTCCGCGCGCTGCTCTGA 1054

## RESULT 7

ADRS5790

ID ADRS5790 standard; DNA; 1054 BP.

XX AC ADRS5790;

XX DT 18-NOV-2004 (first entry)

XX DE Choristoneura fumiferana EcR gene regulated by diacylhydrazine ligand.

XX KW ds; cytostatic; gene therapy; diacylhydrazine ligand;  
XX KW gene expression modulation; ecdysone receptor; functional genomics;  
XX KW proteomics; metabolomics; transgenic organism; cancer therapy;  
XX KW genetic disorder.

XX OS Choristoneura fumiferana.

XX PN W02004072254-A2.

XX XX 26-AUG-2004.

XX XX 10-FEB-2004; 2004WO-US003775.

XX XX 10-FEB-2003; 2003US-0446233P.

XX XX 09-FEB-2004; 2004US-00775883.

XX PA (NEW-) NEW RHEOGENE LLC.

XX PI Hormann RE, Tice CM, Chortyk O, Smith H, Meteyer T;

XX XX WPI; 2004-642299/62.

XX XX Novel diacylhydrazine ligands, useful for modulating expression of  
XX XX exogenous genes in plants or mammals through ecdysone receptor complex.

XX XX Example 2; SEQ ID NO 1; 120pp; English.

PS

XX

CC The invention relates to novel diacylhydrazine ligands (I). (I) is useful  
CC for modulating expression of target gene in host cell, modulating or  
CC expression of one or more exogenous genes, regulating endogenous or  
CC heterologous gene expression in transgenic subject by contacting (I) with  
CC ecdysone receptor complex within cells of subject, where formation of  
CC ecdysone receptor complex-(I)-DNA binding sequence complex induces  
CC expression of gene. (I) is useful in gene therapy, large scale production  
CC of proteins and antibodies, cell-based high throughput screening assays,  
CC functional genomics, proteomics, metabolomics, and regulation of traits  
CC in transgenic organism, where control of gene expression is desired and  
CC for modulating the expression of genes that encode biologically active  
CC proteins of interest, such as secondary proteins, genes that encode e.g.  
CC blood clotting factors, hormones, enzymes, inhibitor substances and genes  
CC useful in cancer therapy and treatment of genetic disorders. (I) is non-  
CC steroidal ligand useful in nuclear receptor-based inducible gene  
CC expression system. (I) is effective in controlling gene expression and  
CC enables regulation of metabolism and to tailor expression levels to suit  
CC the users requirements. This sequence represents an example of a gene  
CC regulated by the compounds of the invention.

XX SQ Sequence 1054 BP; 258 A; 318 C; 273 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 1054; DB 13; Length 1054;

Best Local Similarity 100.0%; Pred. No. 1.5e-281;

Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAGAGAAAGCAAGCAAG 60

Db 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAGAGAAAGCAAGCAAG 60

Qy 61 AAGGAGAAGGACAAATGCTGTGACGACGACGCGTGGACGACCATGCCGCCCATTT 120

Db 61 AAGGAGAAGGACAAATGCTGTGACGACGACGCGTGGACGACCATGCCGCCCATTT 120

Qy 121 ATGCAAGTGAACCTCCACCTCTCTGAGCAGCAAGGATTCACGAAGTGGTCCCAAGGTTT 180

Db 121 ATGCAAGTGAACCTCCACCTCTCTGAGCAGCAAGGATTCACGAAGTGGTCCCAAGGTTT 180

Qy 181 CTCTCGACAAAGCTGTTGGAGACAAACCGGCAGAAAAAATCCCCAGTTTGACAGCCCAAC 240

Db 181 CTCTCGACAAAGCTGTTGGAGACAAACCGGCAGAAAAAATCCCCAGTTTGACAGCCCAAC 240

Qy 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGTACAGGACGGGTACGAGCAGCCTTCTGAT 300

Db 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGTGTACAGGACGGGTACGAGCAGCCTTCTGAT 300

Qy 301 GAAGATTGAAGAGATTACGCGACGCTGGCAGCAAGCGGACGATGAAACGAAAGATCT 360

Db 301 GAAGATTGAAGAGATTACGCGACGCTGGCAGCAAGCGGACGATGAAACGAAAGATCT 360

Qy 361 GACACTCCCTTCGCGCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420

Db 361 GACACTCCCTTCGCGCAGATCAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420

Qy 421 TTGCGGAAGGATTCGCGAGGTTTCGCGAGGTTTCGCGAGGTTTCGCGAGGTTTCGCGAG 480

Db 421 TTGCGGAAGGATTCGCGAGGTTTCGCGAGGTTTCGCGAGGTTTCGCGAGGTTTCGCGAG 480

Qy 481 AAGGCTTGTCTCAAGTGAAGTAAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCA 540

Db 481 AAGGCTTGTCTCAAGTGAAGTAAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCA 540

Qy 541 GACAGTGTCTGTTTCGCGAACCAAGCGTACACTCGCGCAACTACCCAGGCTGGC 600

Db 541 GACAGTGTCTGTTTCGCGAACCAAGCGTACACTCGCGCAACTACCCAGGCTGGC 600

Qy 601 ATGCGCTTACCTCATCGAGGATCTACTGCACTTCTGCGGTGTCATGCTCTATGCGGCTTG 660

Db 601 ATGCGCTTACCTCATCGAGGATCTACTGCACTTCTGCGGTGTCATGCTCTATGCGGCTTG 660

Qy 661 GACAACATCCATTACGCGCTGCTCAAGGCTGTGCTCATCTTTTCTGACCGCGCAGGTTG 720

Db 661 GACAACATCCATTACGCGCTGCTCAAGGCTGTGCTCATCTTTTCTGACCGCGCAGGTTG 720

661 GACACATCCATTACGGCTGCTCAGGCTGTGCTCATCTTTTCTGACCGCCAGGTTG 720  
721 GAGCAGCGCACTGGTGGAGAAATCCAGCGTACTACTGTAATAGCTCCGCACTAT 780  
721 GAGCAGCGCACTGGTGGAGAAATCCAGCGTACTACTGTAATAGCTCCGCACTAT 780  
781 ATCTTGAACAGCTGAGCGGCTGGCGGCTTCTCGGTCTATATACGCGAAGATCCTCTCA 840  
781 ATCTTGAACAGCTGAGCGGCTGGCGGCTTCTCGGTCTATATACGCGAAGATCCTCTCA 840  
841 ATCTTCTGTAGCTAGCAGCGCTGGGATGCAAAATCCAAATGTGCAATCTCCCTCAAG 900  
841 ATCTTCTGTAGCTAGCAGCGCTGGGATGCAAAATCCAAATGTGCAATCTCCCTCAAG 900  
901 CTCAGACAGAAAGCTGCGCGCTTCTCTGAGAGATCTGGGATGTGGGGACATGTGCG 960  
901 CTCAGACAGAAAGCTGCGCGCTTCTCTGAGAGATCTGGGATGTGGGGACATGTGCG 960  
961 CACACCCAAACCGCGCTATCTCTGAGTCCCGCAAGATCTCTAGCCCTGCGCGACGC 1020  
961 CACACCCAAACCGCGCTATCTCTGAGTCCCGCAAGATCTCTAGCCCTGCGCGACGC 1020  
1021 ATCGCGATCGCGCTCGCGCGCTGCTCTGA 1054  
1021 ATCGCGATCGCGCTCGCGCGCTGCTCTGA 1054

RESULT 8  
ID ADR90401  
AC ADR90401 standard; DNA; 1054 BP.  
AC ADR90401,  
XX  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX DNA of Spruce budworm wild-type D, E and F domains from ECR, CfEcr-DEF.  
XX  
XX non-steroidal diacylhydrazine ligand; exogenous; ecdysone receptor;  
XX transgenic; gene therapy; agriculture; pesticide; *Bacillus thuringiensis*;  
XX Bt; toxin; ds.  
XX  
XX Choristoneura fumiferana.  
XX  
XX WO2004078924-A2.  
XX  
XX 16-SEP-2004.  
XX  
XX 27-FEB-2004; 2004WO-US005912.  
XX  
XX 28-FEB-2003; 2003US-0455741P.  
XX 26-FEB-2004; 2004US-00787906.  
XX  
XX (RHEO-) RHEOGENE INC.  
XX  
XX Hermann RE, Potter DW, Chortyk O, Tice CM, Carlson GR, Meyer A;  
XX Opie TR,  
XX  
XX WPI; 2004-677108/66.  
XX  
XX New non-steroidal diacylhydrazine ligands useful for modulating ecdysone  
XX nuclear receptor-based inducible gene expression in e.g. gene therapy,  
XX large scale production of proteins and antibodies.  
XX  
XX Example 3; SEQ ID NO 1; 231pp; English.  
XX  
XX The invention relates to a novel non-steroidal diacylhydrazine ligands  
XX for modulating the expression of exogenous genes via an ecdysone receptor  
XX complex. The invention further comprises: a method for modulating the  
XX expression of a target gene in a host cell; a method for modulating the  
XX expression of an exogenous gene(s); a method for regulating endogenous or  
XX heterologous gene expression in a transgenic subject; a method for  
XX modulating the expression of a gene in a host cell; a method for  
XX producing a polypeptide; and preparing a compound of formula as described

CC in the specification. The novel non-steroidal diacylhydrazine ligands are  
CC useful for: modulating the expression of a target gene in a host cell,  
CC modulating the expression of exogenous gene(s), regulating endogenous or  
CC heterologous gene expression in a transgenic subject (e.g. a plant or a  
CC mammal) containing cells comprising an ecdysone receptor complex and a  
CC DNA binding sequence for the ecdysone receptor complex, modulating the  
CC expression of a gene in a host cell, and producing a polypeptide, e.g. in  
CC gene therapy, large-scale production of proteins and antibodies, cell-  
CC based high throughput screening assays, functional genomics, regulation  
CC of traits in transgenic animals, and in agriculture for controlling the  
CC expression of pesticidal proteins such as *Bacillus thuringiensis* (Bt)  
CC toxin. This polynucleotide sequence represents the wild-type D, E and F  
CC domains from a spruce budworm *Choristoneura fumiferana* Ecr for use in the  
CC construction of a gene expression cassette of the invention.  
XX  
SQ Sequence 1054 BP; 258 A; 318 C; 273 G; 205 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1054; DB 13; Length 1054;  
Best Local Similarity 100.0%; Pred. No. 1.5e-281;  
Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTGAGTGGTGTATACCCGAGACTCAGTCCGCATGAAGCGGAAAGAAAGACAG 60  
DB 1 CTTGAGTGGTGTATACCCGAGACTCAGTCCGCATGAAGCGGAAAGAAAGACAG 60  
QY 61 AAGGAGAGACAAACTGCTGTGAGCAGCAGCGGTGAGCACCACATGCCGCCATT 120  
DB 61 AAGGAGAGACAAACTGCTGTGAGCAGCAGCGGTGAGCACCACATGCCGCCATT 120  
QY 121 ATGCACTGTGAACCTCCACTCTCTGAAGCAGCAAGGATTCAGCAAGTGGTCCCAAGGTTT 180  
DB 121 ATGCACTGTGAACCTCCACTCTCTGAAGCAGCAAGGATTCAGCAAGTGGTCCCAAGGTTT 180  
QY 181 CTCTCCGACAAGCTGTTGGAGACAAACCCGCGAGAAAAAATCCCTCCAGTTGACAGCAAC 240  
DB 181 CTCTCCGACAAGCTGTTGGAGACAAACCCGCGAGAAAAAATCCCTCCAGTTGACAGCAAC 240  
QY 241 CAGCAGTCTTATCCGCGAGGCTCATCTGTTACAGGACGGGTACGAGCGCTTCTGAT 300  
DB 241 CAGCAGTCTTATCCGCGAGGCTCATCTGTTACAGGACGGGTACGAGCGCTTCTGAT 300  
QY 301 GAAGATTTGAGAGGATTAACGAGCAGCTGCGCAGCAAGCGGACGATGAAACGAAAGTCT 360  
DB 301 GAAGATTTGAGAGGATTAACGAGCAGCTGCGCAGCAAGCGGACGATGAAACGAAAGTCT 360  
QY 361 GACATCTCTTCCGCGAGATCAAGAGATGACTATCTCTCAAGTCCAACTTATCGTGGAG 420  
DB 361 GACATCTCTTCCGCGAGATCAAGAGATGACTATCTCTCAAGTCCAACTTATCGTGGAG 420  
QY 421 TTCCGGAAGGATTTGCGAGGTTTCCGCAAGATCTCGCAGCTGATCAAAATGCGTCTT 480  
DB 421 TTCCGGAAGGATTTGCGAGGTTTCCGCAAGATCTCGCAGCTGATCAAAATGCGTCTT 480  
QY 481 AAGGCTTGTCTCAAGTCAAGTAAATGATGCTCCGAGTCCGCGAGATACGATGCGGCTCA 540  
DB 481 AAGGCTTGTCTCAAGTCAAGTAAATGATGCTCCGAGTCCGCGAGATACGATGCGGCTCA 540  
QY 541 GACAGTGTCTTGTTCGCGAACAACCAAGCGTACACTTCGCGACAACTACCGAAGGTGGC 600  
DB 541 GACAGTGTCTTGTTCGCGAACAACCAAGCGTACACTTCGCGACAACTACCGAAGGTGGC 600  
QY 601 ATGGCCTACGTCATCCAGGATCTTCTGCACTTCTGCGGTGCGATGACTATGGGTTG 660  
DB 601 ATGGCCTACGTCATCCAGGATCTTCTGCACTTCTGCGGTGCGATGACTATGGGTTG 660  
QY 661 GACACATCCATTATCCGCGTCTGCTGCTCATCTTTTCTGACCGCGCAGGTTG 720  
DB 661 GACACATCCATTATCCGCGTCTGCTGCTCATCTTTTCTGACCGCGCAGGTTG 720  
QY 721 GAGCAGCGCACTGTTGGAGAAATCCAGCGGTACTTACTGAATACGCTCCGCACTAT 780  
DB 721 GAGCAGCGCACTGTTGGAGAAATCCAGCGGTACTTACTGAATACGCTCCGCACTAT 780

QY 781 ATCTGGAACGCTGAGCGGTGCGGGTTCGTCGTCATATACGCGAAGATCCTCTCA 840  
Db 781 ATCTGGAACGCTGAGCGGTGCGGGTTCGTCGTCATATACGCGAAGATCCTCTCA 840  
QY 841 ATCTCTCTGAGCTACGACGCTCGGATGCAAACTCCAACTGTCATCTCCCTCAAG 900  
Db 841 ATCTCTCTGAGCTACGACGCTCGGATGCAAACTCCAACTGTCATCTCCCTCAAG 900  
QY 901 CTCAAGAACGAAAGCTGCGCCCTTTCTCGAGGAGATCTGGGATGTGGCGGACATGTGC 960  
Db 901 CTCAAGAACGAAAGCTGCGCCCTTTCTCGAGGAGATCTGGGATGTGGCGGACATGTGC 960  
QY 961 CACACCCACGCGCGCTATCTCGATGCCCGGACGATCTCTAGCCCTGCGCGGACGC 1020  
Db 961 CACACCCACGCGCGCTATCTCGATGCCCGGACGATCTCTAGCCCTGCGCGGACGC 1020  
QY 1021 ATGCGCGATGCGCGTTCGCGCGGCTGCTCTGA 1054  
Db 1021 ATGCGCGATGCGCGTTCGCGCGGCTGCTCTGA 1054

## RESULT 9

AAS15631  
ID AAS15631 standard; DNA; 1288 BP.

AC AAS15631;

XX 29-JAN-2002 (first entry)

XX Spruce budworm Ecdysone receptor ligand binding domain CfEcrRDEP DNA.

XX Spruce budworm; Ecdysone receptor; Ecr; ligand binding domain; ds;  
KW retinoid X receptor; RXR; DNA-binding domain; transactivation domain;  
KW nuclear receptor; ultraspiracle; gene therapy; protein production;  
KW antibody production; high throughput screening; HTS; transgenic plant;  
KW transgenic animal; CfEcrRDEP.

OS Choristoneura fumiferana.

XX Key Location/Qualifiers

PH 1. 1239

FT CDS

FT /\*tag= a

FT /product= "Ecr ligand binding domain"

FT /partial

FT /note= "No start codon"

XX WO200170816-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009050.

XX 22-MAR-2000; 2000US-0191355P.

XX 20-FEB-2001; 2001US-0269799P.

XX (ROHM ) ROHM & HAAS CO.

XX Palli SR, Kapitskaya MZ, Cress DE;

XX WPI; 2001-656841/75.

XX P-PSDB; AAU10255.

XX Ecdysone and retinoid X receptor based inducible gene expression systems  
PT for use in e.g. gene therapy, large scale production of proteins and cell  
PT -based high-throughput screening assays.

XX Claim 7; Page 88-89; 144pp; English.

XX The invention relates to Ecdysone and retinoid X receptor based inducible  
CC gene expression systems useful for modulating gene expression in host  
CC cells. The gene expression system encodes a polypeptide with a DNA-  
CC binding domain recognizes a response element associated with a gene whose  
CC expression is to be modulated and/or a ligand binding domain (LBD)

CC comprising a LBD from a nuclear receptor and a second gene expression  
CC cassette capable of being expressed in a host cell comprising a  
CC polynucleotide sequence encoding a second polypeptide comprising a trans-  
CC activation domain and/or a LBD comprising a LBD from a nuclear receptor  
CC other than ultraspiracle (USP) (the trans-activation domain is from a  
CC nuclear receptor other than an ecdysone receptor, a retinoid X receptor  
CC or a USP receptor and the LBDs from the first and second polypeptides are  
CC different and dimerize). The ecdysone and retinoid X receptor based  
CC inducible gene expression systems useful for modulating gene expression  
CC in host cells, for use in gene therapy, large scale production of  
CC proteins and antibodies, cell-based high-throughput screening assays  
CC (HTS), functional genomic and regulation of traits in transgenic plants  
CC and animals. The present sequence encodes a Spruce budworm Ecdysone  
CC receptor ligand binding domain for use in an inducible gene expression  
CC system of the invention

XX SQ Sequence 1288 BP; 318 A; 368 C; 346 G; 256 T; 0 U; 0 Other;

Query Match 100.0%; Score 1054; DB 4; Length 1288;

Best Local Similarity 100.0%; Pred. No. 1.6e-281;

Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGAGTGCCTAGTACCCGAGACTCAGTGCCTCATGAAGCGGAAAGAAAGACACAG 60

Db 235 CCTGAGTGCCTAGTACCCGAGACTCAGTGCCTCATGAAGCGGAAAGAAAGACACAG 294

QY 61 AAGGAGAAGACAAACTGCTGTGACACGACGCGTGACACCATGCGGCCCATTT 120

Db 295 AAGGAGAAGACAAACTGCTGTGACACGACGCGTGACACCATGCGGCCCATTT 354

QY 121 ATGCAAGTGAACCTCCACCTCTGAAGCAGCAAGGATTCAGAAAGTGTGCCAAGGTTT 180

Db 355 ATGCAAGTGAACCTCCACCTCTGAAGCAGCAAGGATTCAGAAAGTGTGCCAAGGTTT 414

QY 181 CTCTCCGACAAGCTGTTGGAGACAAACCCGACGAAACATCCCCAGTTTGACAGCCAAC 240

Db 415 CTCTCCGACAAGCTGTTGGAGACAAACCCGACGAAACATCCCCAGTTTGACAGCCAAC 474

QY 241 CAGCAGTTCCTTATTCGCCAGGCTCATCTGTGTACGAGCGGTACGAGCAGCCTTCTGAT 300

Db 475 CAGCAGTTCCTTATTCGCCAGGCTCATCTGTGTACGAGCGGTACGAGCAGCCTTCTGAT 534

QY 301 GAAGATTTGAAGAGGATTCAGCAGAGCTGGCAGCAAGCGGACGATGAAACGAAAGTCT 360

Db 535 GAAGATTTGAAGAGGATTCAGCAGAGCTGGCAGCAAGCGGACGATGAAACGAAAGTCT 594

QY 361 GACACTCCCTTCGCCGACATCAGAGATGACTATCTCAGCGTCCCACTTATCGTGGAG 420

Db 595 GACACTCCCTTCGCCGACATCAGAGATGACTATCTCAGCGTCCCACTTATCGTGGAG 654

QY 421 TTCCGAAAGGATTTGCCAGGTTTCGCCAAGATCTCGCAGCCTGATCAAAATTAAGCTGCTT 480

Db 655 TTCCGAAAGGATTTGCCAGGTTTCGCCAAGATCTCGCAGCCTGATCAAAATTAAGCTGCTT 714

QY 481 AAGGCTTGCTCAAGTGAGGTAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCA 540

Db 715 AAGGCTTGCTCAAGTGAGGTAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCA 774

QY 541 GACAGTGTCTCTGTTCCGGAACCAAGCGGTACCTCGCGCAACATACCGCAAGGCTGCG 600

Db 775 GACAGTGTCTCTGTTCCGGAACCAAGCGGTACCTCGCGCAACATACCGCAAGGCTGCG 834

QY 601 ATGGCCTTACGTCATCAGGATCTACTGCACTTCTGCGGCTGATGATCTCTATGGCGTTG 660

Db 835 ATGGCCTTACGTCATCAGGATCTACTGCACTTCTGCGGCTGATGATCTCTATGGCGTTG 894

QY 661 GACAAATCCATTAACGCTGCTCAGCGCTGTGCTCATCTTTTGTGACCGCGCAGGTTG 720

Db 895 GACAAATCCATTAACGCTGCTCAGCGCTGTGCTCATCTTTTGTGACCGCGCAGGTTG 954

QY 721 GAGCAGCGCAACTGTTGGAGAAATCCAGCGGTACTACTGATAGCTCTCCGATCTAT 780

Db 955 GAGCAGCGCAACTGTTGGAGAAATCCAGCGGTACTACTGATAGCTCTCCGATCTAT 1014



QY 781 ATCTGAAACAGCTGAGCGGTCGGCGGTTCTGTCGGTCATATACGGCAGATCCTCTCA 840  
 Db 1015 ATCTGAAACAGCTGAGCGGTCGGCGGTTCTGTCGGTCATATACGGCAGATCCTCTCA 1074  
 QY 841 ATCTCTCTGAGCTAGCGAGCTCGGCATGCAAACTCCAAATCTCCAAATGTCATCTCCCTCAAG 900  
 Db 1075 ATCTCTCTGAGCTAGCGAGCTCGGCATGCAAACTCCAAATGTCATCTCCCTCAAG 1134  
 QY 901 CTCAGAACAGAAAGCTGCGGCTTTCTCTCGAGGAGATCTGGGATGTGGCGGACATGTGCG 960  
 Db 1135 CTCAGAACAGAAAGCTGCGGCTTTCTCTCGAGGAGATCTGGGATGTGGCGGACATGTGCG 1194  
 QY 961 CACACCCACCGCGGCTATCTCGAGTCCGCCACGAATCTTAGGCCCTGCGCGCACGC 1020  
 Db 1195 CACACCCACCGCGGCTATCTCGAGTCCGCCACGAATCTTAGGCCCTGCGCGCACGC 1254  
 QY 1021 ATCGCGATGCGCGGTCGGCGGCTGCTCTGA 1054  
 Db 1255 ATCGCGATGCGCGGTCGGCGGCTGCTCTGA 1288

RESULT 10

ID ABS68144 standard; DNA; 1288 BP.  
 AC ABS68144;  
 XX

DT 18-NOV-2002 (first entry)  
 XX

DE DNA encoding ecdysone receptor ligand binding domain #5.  
 XX

XX Gene expression modulation system; DNA-binding domain; ecdysone receptor;  
 KW ligand binding domain; retinoid X receptor; RXR; transactivation domain;  
 KW gene therapy; large-scale production of protein; antibody production;  
 KW functional genomic; transgenic animal; ds.  
 XX

OS Choristoneura fumiferana.  
 XX

XX WO20026614-A2.  
 PN

XX 29-AUG-2002.  
 PD

XX 20-FEB-2002; 2002WO-US005706.  
 PP

XX 20-FEB-2001; 2001US-0269799P.  
 PR

XX 31-MAY-2001; 2001US-0294814P.  
 PR

XX 31-MAY-2001; 2001US-0294819P.  
 PR

XX (ROHM ) ROHM & HAAS CO.  
 PA

XX Palli SR, Kapit'skaya MZ;  
 PI

XX WPI; 2002-674930/72.  
 DR

XX P-PSDB; ABG92569.  
 DR

XX Novel ecdysone receptor/chimeric retinoid X receptor-based inducible gene  
 PT expression system useful for modulating gene expression in a host cell  
 PT for gene therapy and large-scale production of proteins and antibodies.  
 XX

XX Claim 4; Page 127-128; 140pp; English.  
 PS

XX The invention describes a gene expression modulation system (I)  
 CC comprising first and second gene expression cassettes that comprise  
 CC polynucleotides encoding first and second hybrid polypeptides (P1,P2). P1  
 CC comprises a DNA-binding domain and an ecdysone receptor ligand binding  
 CC domain or DNA-binding domain and a chimeric retinoid X receptor (RXR)  
 CC ligand binding domain. P2 comprises a transactivation domain and RXR  
 CC ligand binding domain or transactivation domain and ecdysone receptor  
 CC ligand binding domain. (I) is useful for modulating the expression of a  
 CC gene in a host cell, for applications such as gene therapy, large-scale  
 CC production of proteins and antibodies, cell-based high throughput  
 CC screening assays, functional genomics and regulation of traits in

CC transgenic organisms. This sequence encodes an ecdysone receptor ligand  
 CC binding domain useful in the creation of the gene expression modulation  
 CC system  
 XX  
 SQ Sequence 1288 BP; 318 A; 368 C; 346 G; 256 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1054; DB 6; Length 1288;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-281; Indels 0; Gaps 0;  
 Matches 1054; Conservative 0; Mismatches 0;  
 QY 1 CTTGAGTGGTGTAGTACCCGAGACTCAGTGGCCATGAGCGGAAAGAGAAAGACACAG 60  
 Db 235 CTTGAGTGGTGTAGTACCCGAGACTCAGTGGCCATGAGCGGAAAGAGAAAGACACAG 294  
 QY 61 AAGGAGAGGACAAATCTGCTGTTCAGACGACGAGCGGTGGACCAATGCGGCCATTT 120  
 Db 295 AAGGAGAGGACAAATCTGCTGTTCAGACGACGAGCGGTGGACCAATGCGGCCATTT 354  
 QY 121 ATGCAAGTGTGAACCTCCACCTCTCTGAGCAGCAGAGATTCACGAGTGGTCCCAAGGTTT 180  
 Db 355 ATGCAAGTGTGAACCTCCACCTCTCTGAGCAGCAGAGATTCACGAGTGGTCCCAAGGTTT 414  
 QY 181 CTCTCCGACAAAGCTGTTGGAGACAAACCGGCAGAAAAACATCCCCCAGTTTGACAGCAAC 240  
 Db 415 CTCTCCGACAAAGCTGTTGGAGACAAACCGGCAGAAAAACATCCCCCAGTTTGACAGCAAC 474  
 QY 241 CAGCAGTTCCTTATGCGCAGGCTCATCTGTTACAGGACGCGGTACAGCAGGCTTCAT 300  
 Db 475 CAGCAGTTCCTTATGCGCAGGCTCATCTGTTACAGGACGCGGTACAGCAGGCTTCAT 534  
 QY 301 GAAGATTTGAAGAGGATTAAGCAGAGCTGGCAGACGCGGACGAGTGAAGAGAGTCT 360  
 Db 535 GAAGATTTGAAGAGGATTAAGCAGAGCTGGCAGACGCGGACGAGTGAAGAGAGTCT 594  
 QY 361 GACATCTCCCTTCGCGCAGATTCACAGAGATGACTATCTCAGCGTCAACTTATCTGCGGAG 420  
 Db 595 GACATCTCCCTTCGCGCAGATTCACAGAGATGACTATCTCAGCGTCAACTTATCTGCGGAG 554  
 QY 421 TTCGGAAGGAGATTGCGCAGGTTTCGCAAGATCTTCGACGCTGATCAAAATAGCTGCTT 480  
 Db 655 TTCGGAAGGAGATTGCGCAGGTTTCGCAAGATCTTCGACGCTGATCAAAATAGCTGCTT 714  
 QY 481 AAGGCTTGTCTCAAGTGAAGTGAATGATCTCGAGTTCGCGGACGAGTACGATGGGCTCA 540  
 Db 715 AAGGCTTGTCTCAAGTGAAGTGAATGATCTCGAGTTCGCGGACGAGTACGATGGGCTCA 774  
 QY 541 GACAGTGTCTTGTTCGCGAACAACCAAGCGTACACCTCGCGACAACTACCGCAAGGCTGGC 600  
 Db 775 GACAGTGTCTTGTTCGCGAACAACCAAGCGTACACCTCGCGACAACTACCGCAAGGCTGGC 834  
 QY 601 ATGGCTTACGTATCGAGGATCTATGCACTTTCGCGGTGCGATGATCTTATGGCGTTG 660  
 Db 835 ATGGCTTACGTATCGAGGATCTATGCACTTTCGCGGTGCGATGATCTTATGGCGTTG 894  
 QY 661 GACAAATCATTCAGCGCTGCTCAAGGCTGTGCTCATCTTTTCTGACCGGCGAGGTTG 720  
 Db 895 GACAAATCATTCAGCGCTGCTCAAGGCTGTGCTCATCTTTTCTGACCGGCGAGGTTG 954  
 QY 721 GAGCAGCGCAACTGCTGGAAGAAATTCAGCGGTACTTACTGAAATACGCTCCGCACTCAT 780  
 Db 955 GAGCAGCGCAACTGCTGGAAGAAATTCAGCGGTACTTACTGAAATACGCTCCGCACTCAT 1014  
 QY 781 ATCTGAAACAGCTGAGCGGTCGGCGGTTCTGCTGCGTATATACGGCAGATCCTCTCA 840  
 Db 1015 ATCTGAAACAGCTGAGCGGTCGGCGGTTCTGCTGCGTATATACGGCAGATCCTCTCA 1074  
 QY 841 ATCTCTCTGAGCTAGCGAGCTCGGCATGCAAACTCCAAATGTCATCTCCCTCAAG 900  
 Db 1075 ATCTCTCTGAGCTAGCGAGCTCGGCATGCAAACTCCAAATGTCATCTCCCTCAAG 1134  
 QY 901 CTCAGAACAGAAAGCTGCGGCTTTCTCTCGAGGAGATCTGGGATGTGGCGGACATGTGCG 960  
 Db 1135 CTCAGAACAGAAAGCTGCGGCTTTCTCTCGAGGAGATCTGGGATGTGGCGGACATGTGCG 1194



QY 961 CACACCCAAACCGCGCTATCTCGAGTCCCCCAAGAAATCTTAGCCCTCGCGCACGC 1020  
 DB 1195 CACACCCAAACCGCGCTATCTCGAGTCCCCCAAGAAATCTTAGCCCTCGCGCACGC 1254  
 QY 1021 ATGCGCGATCGCGGCTCGCGCGCGCTGCTCTGA 1054  
 DB 1255 ATGCGCGATCGCGGCTCGCGCGCGCTGCTCTGA 1288

RESULT 11  
 ABT08298  
 ID ABT08298 standard; DNA; 1288 BP.  
 XX  
 AC  
 XX  
 AC  
 XX  
 DT 28-NOV-2002 (first entry)  
 XX  
 DE BCR-based inducible gene expression cassette related DNA SEQ ID No 45.  
 KW Gene expression modulation system; large-scale production; gene therapy;  
 KW Gene expression cassette; functional genomics; transgenic organism; ds.  
 XX  
 XX Choriostoneura fumiferana.  
 XX  
 PN WO200266613-A2.  
 XX  
 PD 29-AUG-2002.  
 XX  
 PF 20-FEB-2002; 2002WO-US005235.  
 XX  
 PR 20-FEB-2001; 2001US-0269799P.  
 PR 31-MAY-2001; 2001US-0294814P.  
 XX  
 XX (ROHM ) ROHM & HAAS CO.  
 PA  
 PI Palli SR, Kapitskaya MZ;  
 XX  
 DR WPI; 2002-674929/72.  
 XX  
 PT Novel ecdysone receptor/invertebrate retinoid X receptor-based inducible  
 PT gene expression system useful for modulating gene expression in host cell  
 PT for gene therapy and large-scale production of proteins and antibodies.  
 XX  
 PS Claim 4; Page 112; 123pp; English.  
 XX  
 CC The invention relates to a novel gene expression modulation system  
 CC comprising first and second gene expression cassettes that comprises  
 CC polynucleotides encoding first and second hybrid polypeptides. The gene  
 CC expression modulation system is useful for modulating the expression of a  
 CC gene in a host cell comprising the gene to be modulated, for applications  
 CC such as gene therapy, large-scale production of proteins and antibodies,  
 CC cell-based high throughput screening assays, functional genomics and  
 CC regulation of traits in transgenic organisms. This polynucleotide  
 CC sequence represents DNA relating to the gene expression cassettes of the  
 CC invention  
 XX  
 SQ Sequence 1288 BP; 318 A; 368 C; 346 G; 256 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1054; DB 6; Length 1288;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-281;  
 Matches 1054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGAGTGGCTAGTACCGGAGCTCAGTGGCCATGAAGCGGAGAGAGAGACACAG 60  
 DB 235 CCTGAGTGGCTAGTACCGGAGCTCAGTGGCCATGAAGCGGAGAGAGAGACACAG 294  
 QY 61 AAGGAGAGAGACAACTGCGCTGTGACGACGACGCTGGACGACACATGCGCCCATTT 120  
 DB 295 AAGGAGAGAGACAACTGCGCTGTGACGACGACGCTGGACGACACATGCGCCCATTT 354  
 QY 121 ATGCAGTGTGAACCTCCACTCTCTGAAAGAGAGAGAGATTCAAGAGTGGTCCCAAGTTT 180

DB 355 ATGCAGTGTGAACCTCCACTCTGTAAGCAGCAAGATTCAAGAGTGGTCCCAAGGTTT 414  
 QY 181 CTCTCCGACAAAGCTGTGTGAGACAAACCGCGCAGAAAAAATCCATCCCGAGTTTGACAGCAAC 240  
 DB 415 CTCTCCGACAAAGCTGTGTGAGACAAACCGCGCAGAAAAAATCCATCCCGAGTTTGACAGCAAC 474  
 QY 241 CAGCAGTTCTTATTCGCCAGGCTCATCTGGTACACGAGACGGGTACGAGCAGCCTTCTGAT 300  
 DB 475 CAGCAGTTCTTATTCGCCAGGCTCATCTGGTACACGAGACGGGTACGAGCAGCCTTCTGAT 534  
 QY 301 GAGATTTTGAAGAGGATTACGACAGAGCTGCGACAGCGGACGATGAAACGAGAGTCT 360  
 DB 535 GAAGATTTGAAGAGGATTACGACAGAGCTGCGACAGCGGACGATGAAACGAGAGTCT 594  
 QY 361 GACACTCCCTTTCGCCAGATCAAGAGATGACTATCTCTCAGCGTCCAACTTATCTGGAG 420  
 DB 595 GACACTCCCTTTCGCCAGATCAAGAGATGACTATCTCTCAGCGTCCAACTTATCTGGAG 654  
 QY 421 TTCCGAGAGGATTGCGAGGTTTGGCCAGATCTCGAGGCTGATCAAAATACGCTGCTT 480  
 DB 655 TTCCGAGAGGATTGCGAGGTTTGGCCAGATCTCGAGGCTGATCAAAATACGCTGCTT 714  
 QY 481 AAGGCTTGTCTCAAGTCAAGTGAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCA 540  
 DB 715 AAGGCTTGTCTCAAGTCAAGTGAATGATGCTCCGAGTCCGCGACGATACGATGCGGCTCA 774  
 QY 541 GACAGTGTCTTCTGTTCCGCAACAAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 600  
 DB 775 GACAGTGTCTTCTGTTCCGCAACAAACCAAGCGTACACTCGCGACAACTACCGCAAGGCTGGC 834  
 QY 601 ATGGCTTACGTCATCGAGGATCTACTGCACTTCTGCGGTGCACTGATCTCTATGGCGTTG 660  
 DB 835 ATGGCTTACGTCATCGAGGATCTACTGCACTTCTGCGGTGCACTGATCTCTATGGCGTTG 894  
 QY 661 GACAAATCCATTAACGCGTCTCAGCGCTGCTCATCTTTTCTGACCGCGCAGGTTG 720  
 DB 895 GACAAATCCATTAACGCGTCTCAGCGCTGCTCATCTTTTCTGACCGCGCAGGTTG 954  
 QY 721 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACTGAATACGCTCCGCACTAT 780  
 DB 955 GAGCAGCGCAACTGGTGGAGAAATCCAGCGGTACTACTGAATACGCTCCGCACTAT 1014  
 QY 781 ATCTGAAACAGCTGAGCGGCTCGCGGCTTCTGCGTCAATATACGCGCAAGATCTCTCA 840  
 DB 1015 ATCTGAAACAGCTGAGCGGCTCGCGGCTTCTGCGTCAATATACGCGCAAGATCTCTCA 1074  
 QY 841 ATCTCTCTGAGCTAGCAGCTCGCGCTCGCAAACTCCAACTGTCATCTCCCTCAAG 900  
 DB 1075 ATCTCTCTGAGCTAGCAGCTCGCGCTCGCAAACTCCAACTGTCATCTCCCTCAAG 1134  
 QY 901 CTCAGAGAACAAAGCTGCGGCTTCTCTCGAGGAGATCTGGGATGTGGCGGACATGTCG 960  
 DB 1135 CTCAGAGAACAAAGCTGCGGCTTCTCTCGAGGAGATCTGGGATGTGGCGGACATGTCG 1194  
 QY 961 CACACCCAAACCGCGCTATCTCTGAGTCCCGCAGCAATCTTAGCCCTCGCGGACGC 1020  
 DB 1195 CACACCCAAACCGCGCTATCTCTGAGTCCCGCAGCAATCTTAGCCCTCGCGGACGC 1254  
 QY 1021 ATGCGCGATCGCGGCTCGCGCGCGCTGCTCTGA 1054  
 DB 1255 ATGCGCGATCGCGGCTCGCGCGCGCTGCTCTGA 1288

RESULT 12  
 ABK49451  
 ID ABK49451 standard; DNA; 1290 BP.  
 XX  
 AC  
 XX  
 AC  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE DNA encoding Choriostoneura fumiferana ecdysone receptor (CEBcr) #1.  
 XX

KW Ecdysone; receptor; EcR; multiple inducible gene modulation system;  
 KW proteomic; functional genomic; gene therapy; toxicology screening;  
 KW large scale protein production; transactivation; biosensor;  
 KW spruce budworm; ds.

XX Choristoneura fumiferana.

XX WO200229075-A2.

XX 11-APR-2002.

XX 28-SEP-2001; 2001WO-US030608.

XX 03-OCT-2000; 2000US-0237446P.

XX 27-SEP-2001; 2001US-00965697.

XX (ROHM ) ROHM & HAAS CO.

XX Dhadialla TS, Cress DE, Carlson GR, Hormann RE, Palli SR;

PI Kudla AJ, Herzig RP, Philip M;

XX WPI; 2002-352234/38.

XX A multiple inducible gene modulation system, for investigating multi-gene  
 PT processes, comprises several individually operable gene modulation  
 PT systems.

PS Example 1; Page 71; 79pp; English.

CC The invention describes a multiple inducible gene modulation system (I)  
 CC comprising several individually operable gene modulation systems. It also  
 CC useful in proteomics, functional genomics, gene therapy, cell-based high  
 CC throughput assays, biosensors, toxicology screening and large scale  
 CC protein production. Specifically, it allows investigation of complex  
 CC multi-gene processes such as signal transduction cascades. It also  
 CC enables regulation of multiple genes for gene therapy. In (I), because  
 CC the binding and transactivation domains reside on two different  
 CC molecules, the background activity in the absence of ligand is greatly  
 CC reduced. It also provides improved sensitivity to non-steroidal ligands.  
 CC Also since transactivation based on ecdysone receptor switches is  
 CC cell-line dependent, it is easier to tailor switching systems to obtain  
 CC maximum transactivation capability for each application. This sequence  
 CC encodes the Choristoneura fumiferana ecdysone receptor (CfEcR) C (DNA  
 CC binding), D (hinge), E (ligand binding) and F domains used in the  
 CC creation of a gene expression cassette for use in the multiple inducible  
 CC gene expression system

XX Sequence 1290 BP; 321 A; 364 C; 347 G; 258 T; 0 U; 0 Other;

Query Match 97.78; Score 1029.4; DB 6; Length 1290;

Best Local Similarity 99.74; Pred. No. 1e-274;

Matches 1052; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 60  
 DB |||||  
 QY 237 CCTGAGTGGCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAAGAGAAAGACACAG 296  
 DB |||||  
 QY 61 AAGGAGAAGGACAACTGCTGTGACGACGACGAGCGGTGGACACCATGCGCCCATTT 120  
 DB |||||  
 QY 297 AAGGAGAAGGACAACTGCTGTGACGACGACGAGCGGTGGACACCATGCGCCCATTT 356  
 DB |||||  
 QY 121 ATGCGAGTGTGAACCTTCCACTCTGGAAGCAGCAAGGATTCACGAGTGGTCCCAAGTTT 180  
 DB |||||  
 QY 357 ATGCGAGTGTGAACCTTCCACTCTGGAAGCAGCAAGGATTCACGAGTGGTTCGAAGTTT 416  
 DB |||||  
 QY 181 CTCTCCGACAAAGCTGTGGAGACAAACCGGACGAAAAACATCCCGCAGTTTGACAGCCAAC 240  
 DB |||||  
 QY 417 CTCTCCGACAAAGCTGTGGAGACAAACCGGACGAAAAACATCCCGCAGTTTGACAGCCAAC 476  
 DB |||||  
 QY 241 CAGCAGTTCCTTATCGCCAGGCTCATCTGGTACGAGCCGGTACGAGCCGCTTCTGAT 300  
 DB |||||  
 QY 477 CAGCAGTTCCTTATCGCCAGGCTCATCTGGTACGAGCCGGTACGAGCCGCTTCTGAT 536  
 DB |||||

QY 301 GAAGATTTTCAAGGATTACGACAGCTGGCGGACGAGCGGACGATGATCAAAACGAGAGTCT 360  
 DB |||||  
 QY 537 GAAGATTTTCAAGGATTACGACAGCTGGCGGACGAGCGGACGATGATCAAAACGAGAGTCT 596  
 DB |||||  
 QY 361 GACATCTCCCTTCCGCGCAGATCACAGAGATGACTATCTCACGCTCCAACTTATCGTGGAG 420  
 DB |||||  
 QY 597 GACATCTCCCTTCCGCGCAGATCACAGAGATGACTATCTCACGCTCCAACTTATCGTGGAG 656  
 DB |||||  
 QY 421 TTGCGGAAAGGATTTCCAGGGTTCCGCAAGATCTCGACGCTGATCAAAATACGCTGCTT 480  
 DB |||||  
 QY 657 TTGCGGAAAGGATTTCCAGGGTTCCGCAAGATCTCGACGCTGATCAAAATACGCTGCTT 716  
 DB |||||  
 QY 481 AAGGCTTGTCTCAAGTGAGTGAATGATCTCCGAGTCCGCGGACGATACGATCGGCTCA 540  
 DB |||||  
 QY 717 AAGGCTTGTCTCAAGTGAGTGAATGATCTCCGAGTCCGCGGACGATACGATCGGCTCA 776  
 DB |||||  
 QY 541 GACAGTGTCTCTGTTCCGCGAAACCAACGAGTGTACACTCCGCGACAACTACCGCAAGGCTGGC 600  
 DB |||||  
 QY 777 GACAGTGTCTCTGTTCCGCGAAACCAACGAGTGTACACTCCGCGACAACTACCGCAAGGCTGGC 836  
 DB |||||  
 QY 601 ATGGCTTACGTCATCGAGGATCTATGCACTTCTGCGGTGATGATCTATGCGGTTG 660  
 DB |||||  
 QY 837 ATGGCTTACGTCATCGAGGATCTATGCACTTCTGCGGTGATGATCTATGCGGTTG 896  
 DB |||||  
 QY 661 GACAACTCATTTAGCGCTGTCTACGCGTGTCTGCGGTGATGATCTATGCGGTTG 720  
 DB |||||  
 QY 897 GACAACTCATTTAGCGCTGTCTACGCGTGTCTGCGGTGATGATCTATGCGGTTG 956  
 DB |||||  
 QY 721 GACAGCCGCAACTGGTGGAAAGAAATCCAGCGGTACTACTGAAATACGCTCCGCACTTAT 780  
 DB |||||  
 QY 957 GACAGCCGCAACTGGTGGAAAGAAATCCAGCGGTACTACTGAAATACGCTCCGCACTTAT 1016  
 DB |||||  
 QY 781 ATCTGAAACAGCTGAGCGGTGCGCGCTTCTGCGTCAATATACGCGCAAGATCTCTCTCA 840  
 DB |||||  
 QY 1017 ATCTGAAACAGCTGAGCGGTGCGCGCTTCTGCGTCAATATACGCGCAAGATCTCTCTCA 1076  
 DB |||||  
 QY 841 ATCTCTCTGAGCTACGCAAGCTGGGATGCAAACTCCAAACATGTCATCTCCCTCAAG 900  
 DB |||||  
 QY 1077 ATCTCTCTGAGCTACGCAAGCTGGGATGCAAACTCCAAACATGTCATCTCCCTCAAG 1136  
 DB |||||  
 QY 901 CTCAAGACAGAAAGCTGCGCGCTTCTCTCGAGGAGATCTGGGATGTGGC-GGACATGTC 959  
 DB |||||  
 QY 1137 CTCAAGACAGAAAGCTGCGCGCTTCTCTCGAGGAGATCTGGGATGTGGCAGGACATGTC 1196  
 DB |||||  
 QY 960 GCACACCCAAACCGCCCTTATCTCGAGTCCCGCCACGAATCTCTAGCCCTTGGCGCACG 1019  
 DB |||||  
 QY 1197 GCACACCCAAACCGCCCTTAT-CTCGAGTCCCGCCACGAATCTCTAGCCCTTGGCGCACG 1255  
 DB |||||  
 QY 1020 CATCGCGGATGCGCGTCCGCGCGCTGCTCTGA 1054  
 DB |||||  
 QY 1256 CATCGCGGATGCGCGTCCGCGCGCTGCTCTGA 1290  
 DB |||||

RESULT 13

ACF36056

ID ACF36056 standard; DNA; 1290 BP.

XX ACF36056;

XX AC

XX 20-NOV-2003 (first entry)

XX

DE C. fumiferana ecdysone receptor (EcR) C, D, E and F domains DNA sequence.

XX GAL4; DNA binding domain; DBD; gene expression; gene switch; EcR;

KW ecdysone receptor; ds.

XX Choristoneura fumiferana.

OS WO2003060103-A2.

PN 24-JUL-2003.

XX 13-JAN-2003; 2003WO-US000915.

XX

PF

XX	14-JAN-2002; 2002US-0348427P.	
XX	(ROHM ) ROHM & HAAS CO.	
XX	Palli SR;	
XX	WPI; 2003-618180/58.	
XX	Novel minimal DNA binding domain polypeptide useful for regulating gene expression in host cell.	
XX	Example 1; Page 66-67; 72pp; English.	
XX	The invention relates to a minimal GAL4 DNA binding domain (DBD) polypeptide (I). The encoding polynucleotide (II) is useful in gene expression system. An isolated host cell transfected with a vector comprising (II) is useful for preparing (I) by recombinant techniques. (I) and (II) is also useful in gene switch systems and also to modulate gene expression in host cell, where the gene encodes enzymes like alpha - amylase, phytase, and genes for resistance against insects, nematodes, fungi, bacteria, viruses, and abiotic stresses, antigens, nutraceuticals, pharmaceuticals, vitamins, genes for modifying amino acid content, herbicide resistance, cold, drought, and heat tolerance, industrial products, oils, protein, carbohydrates, antioxidants, male sterile plants, flowers, fuels, therapeutic polypeptides, pathway intermediates, for the modulation of pathways already existing in the host for the synthesis of new products, cell based assays; functional genomics assays, biotherapeutic protein production, proteomics assays. The present sequence represents a C. fumiferana ecdysone receptor (EcR) C, D, E and F domains encoding DNA sequence, used in the construction of GAL4 variants	
XX	SQ Sequence 1290 BP; 321 A; 364 C; 347 G; 258 T; 0 U; 0 Other;	
XX	Query Match 97.78; Score 1029.4; DB 9; Length 1290;	
XX	Best Local Similarity 99.78; Pred. No. 1e-274;	
XX	Matches 1052; Conservative 0; Mismatches 1; Indels 2; Gaps 2;	
QY	1 CCTGAGTGCCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAGAGAAAGACACAG 60	
DB		
DB	237 CCTGAGTGCCTAGTACCCGAGACTCAGTGGCCATGAAGCGGAAGAGAAAGACACAG 296	
QY	61 AAGGAGAAGACAAATGCTCTGTGACGACGACGAGGAGACCAATGCCGCCATT 120	
DB		
DB	297 AAGGAGAAGACAAATGCTCTGTGACGACGACGAGGAGACCAATGCCGCCATT 356	
QY	121 ATGCAAGTGAACCTCACTCTGAGACGACGAGGATTCAGAGTGGTCCCAAGTTT 180	
DB		
DB	357 ATGCAAGTGAACCTCACTCTGAGACGACGAGGATTCAGAGTGGTCCCAAGTTT 416	
QY	181 CTCTCCGACAAAGCTGTTGGAGACAAACCGGACGAGAAACATCCCCAGTTGACAGCCAAC 240	
DB		
DB	417 CTCTCCGACAAAGCTGTTGGAGACAAACCGGACGAGAAACATCCCCAGTTGACAGCCAAC 476	
QY	241 CAGCAGTTCTTATCGCCAGGCTCATCTGTGACGACGAGGATTCAGAGCCCTTCGTAT 300	
DB		
DB	477 CAGCAGTTCTTATCGCCAGGCTCATCTGTGACGACGAGGATTCAGAGCCCTTCGTAT 536	
QY	301 GAGATTTGAAGAGGATTACGACAGCTGCGACGACGACGAGTGAACGAGAGTCT 360	
DB		
DB	537 GAGATTTGAAGAGGATTACGACAGCTGCGACGACGACGAGTGAACGAGAGTCT 596	
QY	361 GACACTCCCTTCGCCAGATCACAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 420	
DB		
DB	597 GACACTCCCTTCGCCAGATCACAGAGATGACTATCTCAGCGTCCAACTTATCGTGGAG 656	
QY	421 TTCGCGAAGGATTGCCAGGTTGCCCAAGATCTCGCAGGCTGATCAAAATTCGCTGCTT 480	
DB		
DB	657 TTCGCGAAGGATTGCCAGGTTGCCCAAGATCTCGCAGGCTGATCAAAATTCGCTGCTT 716	
QY	481 AAGCTTGCTCAAGTAGGTAATGATGCTCCGAGTCCGCGACGATACGATGCGGCCCTCA 540	
DB		
DB	717 AAGCTTGCTCAAGTAGGTAATGATGCTCCGAGTCCGCGACGATACGATGCGGCCCTCA 776	
QY	541 GACAGTGTCTGTTCGCGAACAACCAAGCGGTACACTCGCGACAACCTACCGCAAGGCTGGC 600	
DB		
DB	777 GACAGTGTCTGTTCGCGAACAACCAAGCGGTACACTCGCGACAACCTACCGCAAGGCTGGC 836	
QY	601 ATGGCCCTACGTCAATCGAGGATCTACTGCACCTTCTGCGGTCGATGATCTTATGGCGTTG 660	
DB		
DB	837 ATGGCCCTACGTCAATCGAGGATCTACTGCACCTTCTGCGGTCGATGATCTTATGGCGTTG 896	
QY	661 GACAAATCATTACCGCTGCTCAGCGGTGTCGATCATCTTTTCTGACCGGCGAGGTTG 720	
DB		
DB	897 GACAAATCATTACCGCTGCTCAGCGGTGTCGATCATCTTTTCTGACCGGCGAGGTTG 956	
QY	721 GACACGCGCAACTGTTGGAAGAAATCCAGCGGTACTACTGTAATAGCTCCGCATCTAT 780	
DB		
DB	957 GACACGCGCAACTGTTGGAAGAAATCCAGCGGTACTACTGTAATAGCTCCGCATCTAT 1016	
QY	781 ATCTGTAACCAAGTGAAGCGGTGCGCGCTTCTGCTCATATACCGCAAGATCTCTCTCA 840	
DB		
DB	1017 ATCTGTAACCAAGTGAAGCGGTGCGCGCTTCTGCTCATATACCGCAAGATCTCTCTCA 1076	
QY	841 ATCTCTCTGAGCTAGCGACGCTCGGCATGCAAAATCTCCAAATGTCATCTCCCTCAAG 900	
DB		
DB	1077 ATCTCTCTGAGCTAGCGACGCTCGGCATGCAAAATCTCCAAATGTCATCTCCCTCAAG 1136	
QY	901 CTCAGAACAAGAAAGCTGCGCTTCTCTGAGGAGATCTGGGATGTGGC-GGACATGTC 959	
DB		
DB	1137 CTCAGAACAAGAAAGCTGCGCTTCTCTGAGGAGATCTGGGATGTGGC-GGACATGTC 1196	
QY	960 GCACACCAACCGCGCTTATCTCGAGTCCCGCCCAAGATCTTAGCCCTGCGCGCAGC 1019	
DB		
DB	1197 GCACACCAACCGCGCTTAT-CTCGAGTCCCGCCCAAGATCTTAGCCCTGCGCGCAGC 1255	
QY	1020 CATCGCGGATGCGCGCTCGCGCGCGCTGCTCTGA 1054	
DB		
DB	1256 CATCGCGGATGCGCGCTCGCGCGCGCTGCTCTGA 1290	
XX	RESULT 14	
XX	ABK49461	
ID	ABK49461 standard; DNA; 1073 BP.	
XX	AC AC	
XX	ABK49461;	
DT	02-JUL-2002 (first entry)	
XX	DNA encoding Choristoneura fumiferana ecdysone receptor (CEEcR) #2.	
DE	Ecdysone; receptor; EcR; multiple inducible gene modulation system;	
XX	proteomic; functional genomic; gene therapy; toxicology screening;	
KW	large scale protein production; transactivation; biosensor;	
KW	spruce budworm; ds.	
XX	Choristoneura fumiferana.	
OS	WO200229075-A2.	
PN	11-APR-2002.	
XX	28-SEP-2001; 2001WO-US030608.	
PF	03-OCT-2000; 2000US-0237446P.	
XX	27-SEP-2001; 2001US-00965697.	
PR	(ROHM ) ROHM & HAAS CO.	
XX	Dhadialla TS, Cress DE, Carlson GR, Hormann RE, Palli SR;	
PI	Kudla AJ, Herzig RP, Philip M;	
XX	WPI; 2002-352234/38.	
DR	A multiple inducible gene modulation system, for investigating multi-gene processes, comprises several individually operable gene modulation	



CC plants, flowers, fuels, therapeutic polypeptides, pathway intermediates,  
CC for the modulation of pathways already existing in the host for the  
CC synthesis of new products, cell based assays; functional genomics assays,  
CC biotherapeutic protein production, proteomics assays. The present  
CC sequence represents a C. fumiferana ecdysone receptor (EcR) related DNA  
CC sequence  
XX  
SQ Sequence 1073 BP; 266 A; 319 C; 275 G; 213 T; 0 U; 0 Other;

Query Match 95.8%; Score 1010.2; DB 9; Length 1073;  
Best Local Similarity 99.2%; Pred. No. 2e-269;  
Matches 1047; Conservative 0; Mismatches 3; Indels 5; Gaps 3;

QY 1 CCTGAGTGGTAGTACCGGAGACTCAGTGGCCCATGAAGCGGAAAGAGAAAGCAAGCAG 60  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1 CCTGAGTGGTAGTACCGGAGACTCAGTGGCCCATGAAGCGGAAAGAGAAAGCAAGCAG 60  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 61 AAGGAGAGGACAACTGCCCTGTCCAGCAGCAGCGTGGACGACCAATGCCGCCCATTT 120  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 61 AAGGAGAGGACAACTGCCCTGTCCAGCAGCAGCGTGGACGACCAATGCCGCCCATTT 120  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 121 ATGCAAGTGTGAACCTCCACCTCTCTGAAGCAGCAAGGATTACAGAAAGTGGTCCCAAGGTTT 180  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 121 ATGCAAGTGTGAACCTCCACCTCTCTGAAGCAGCAAGGATTACAGAAAGTGGTCCCAAGGTTT 180  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 181 CTCTCCGACAAAGCTGTGTGGAGCAAAACCGGAGAAACATCCCCAGTTGACAGCCAAAC 240  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 181 CTCTCCGACAAAGCTGTGTGGAGCAAAACCGGAGAAACATCCCCAGTTGACAGCCAAAC 240  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 241 CAGCAGTTCCTTATCCGCCAGGCTCATCTGGTACGAGCGGTACGAGCGGCTTCTGAT 300  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 241 CAGCAGTTCCTTATCCGCCAGGCTCATCTGGTACGAGCGGTACGAGCGGCTTCTGAT 300  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 301 GAAGATTGAAGAGGATTACGACAGCTGGCAGCAAGCGGACGATGAAACGAAAGAGTCT 360  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 301 GAAGATTGAAGAGGATTACGACAGCTGGCAGCAAGCGGACGATGAAACGAAAGAGTCT 360  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 361 GACACTCCCTTCGCCAGATCAGAGATGATATCTCAGCGGTCCAACTTATCGTGGAG 420  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 361 GACACTCCCTTCGCCAGATCAGAGATGATATCTCAGCGGTCCAACTTATCGTGGAG 420  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 421 TTCCGAGAGGATTCGAGGTTCCGAGGTTCCGAGGTTCCGAGGTTCCGAGGTTCCGAGGTT 480  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 421 TTCCGAGAGGATTCGAGGTTCCGAGGTTCCGAGGTTCCGAGGTTCCGAGGTTCCGAGGTT 480  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 481 AAGGCTTGTCTCAAGTGAAGTAAATGATCTCGAGTCCGAGCGATACGATGCGGCTCA 540  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 481 AAGGCTTGTCTCAAGTGAAGTAAATGATCTCGAGTCCGAGCGATACGATGCGGCTCA 540  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 541 GACAGTGTCTGTTCGCGAAACAAACGAGCTGACCTCGGACAACTACCGCAAGGCTGGC 600  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 541 GACAGTGTCTGTTCGCGAAACAAACGAGCTGACCTCGGACAACTACCGCAAGGCTGGC 600  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 601 ATGCGCTACGTCATGAGGATCTACTGACATCTTCCGCGGTGATGATCTATGCGGTTG 660  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 598 ATGCGCTACGTCATGAGGATCTACTGACATCTTCCGCGGTGATGATCTATGCGGTTG 657  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 661 GACAAATCCATTAACGCGTGTCTCAGCGTGTGCTCATCTTTCTGACCGGCGAGGTTG 720  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 658 GACAAATCCATTAACGCGTGTCTCAGCGTGTGCTCATCTTTCTGACCGGCGAGGTTG 717  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 721 GAGCAGCGCAACTGTGTGGAAGAAATCCAGCGGTACTACCTGAATACGCTCCGATCTAT 780  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 718 GAGCAGCGCAACTGTGTGGAAGAAATCCAGCGGTACTACCTGAATACGCTCCGATCTAT 777  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 781 ATCTGAAACGAGCTGAGCGGTTCGGCGGTTCGTCGATATATACGCGAAGATCTCTCA 840  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 778 ATCTGAAACGAGCTGAGCGGTTCGGCGGTTCGTCGATATATACGCGAAGATCTCTCA 837  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 841 ATCTCTCTGAGCTACGCGAGCTCGGATGCAAAATCCAAACATGTCATCTCCCTCAAG 900  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 838 ATCTCTCTGAGCTACGCGAGCTCGGATGCAAAATCCAAACATGTCATCTCCCTCAAG 897  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 901 CTCAGNACAGAAAGCTGCGCGCTTTCTCGAGAGATCTGGGATGTGGC-GGACATGTC 959  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 898 CTCAGNACAGAAAGCTGCGCGCTTTCTCGAGAGATCTGGGATGTGGCAGGACATGTC 957  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 960 GCACACCCAAACCGCGCTATCTCGAGTCCCGCAGAAATCTTAGCCCTGCGCGCACG 1019  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 958 GCACACCCAAACCGCGCTAT-CTCGAGTCCCGCAGAAATCTTAGCCCTGCGCGCACG 1016  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1020 CATCGCGGATGCGCGCTTCGCGCGGCTGCTCTGA 1054  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1017 CATCGCGGATGCGCGCTTCGCGCGGCTGCTCTGA 1051  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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